

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 24, 2005, 18:26:36 ; Search time 2360 Seconds
(without alignments)
15349.114 Million cell updates/sec

Title: US-10-063-553-47

Perfect score: 766

Sequence: 1 ggctcgagcgttcttgagcc.....agtagttgaaaaaaaaa 766

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_hgt.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	766	100.0	766	6	AR252552
2	766	100.0	766	6	AX092316
3	766	100.0	766	6	AX376130
4	766	100.0	766	6	AX403370
5	766	100.0	766	9	AY358671
6	747	97.5	2308	9	AK026453
7	332	43.3	46778	2	AC079784
8	332	43.3	206624	9	AC097662
9	264.2	34.5	351	6	AX246020
10	231.4	30.2	286	6	AX098190
11	184	24.0	201	6	CQ741848
12	171.6	22.4	203478	10	AC138214
13	168.2	22.0	209326	2	AC106407
14	168.2	22.0	257693	2	AC103323
15	148.6	19.4	378	6	AX246229
16	128.8	16.8	208731	2	AC129037
17	92.8	12.1	308833	2	AC106408
18	60	7.8	60	6	CQ550697
19	50.2	6.6	873	5	BX932079

c	20	49.2	6.4	110000	2	AC112083_1
c	21	48.6	6.3	853	5	BX935444
c	22	46.2	6.0	137088	9	AC135628
c	23	45	5.9	132384	9	AC116347
c	24	45	5.9	168242	9	AC140830
c	25	45	5.9	168430	2	AC145037
c	26	45	5.9	173275	2	AC145031
c	27	45	5.9	175559	2	AC145101
c	28	43.8	5.7	1141	6	AX083744
c	29	43.4	5.7	2000	6	AX655393
c	30	42.4	5.5	181307	5	BX649358
c	31	41	5.4	190499	2	AC068392
c	32	41	5.4	190845	9	AC108695
c	33	40.8	5.3	146479	9	AC097472
c	34	40.8	5.3	191081	2	AC023143
c	35	40.4	5.3	87394	9	HSJ718D20
c	36	40.4	5.3	149310	2	AC148196
c	37	40.2	5.2	107593	2	AC107484
c	38	40.2	5.2	167791	9	AC108075
c	39	39.8	5.2	189968	9	AC007682
c	40	39.6	5.2	263405	2	AC124845
c	41	39.6	5.2	268894	2	AC129448
c	42	39.4	5.1	8031	6	CQ719320
c	43	39.4	5.1	8034	9	HSY16241
c	44	39.2	5.1	1577	9	AK098573
c	45	39.2	5.1	72000	9	AP002958
c	46	39.2	5.1	153733	2	AC011980
c	47	39.2	5.1	159946	2	AC079194
c	48	39.2	5.1	172848	2	AP001532
c	49	39.2	5.1	176680	9	AC090358
c	50	39.2	5.1	178182	2	AP001400
c	51	39.2	5.1	219382	5	BX247881
c	52	39	5.1	193593	2	BX927289
c	53	38.8	5.1	185141	2	AC150601
c	54	38.8	5.1	349980	6	AX344563
c	55	38.6	5.0	150578	2	AC135551
c	56	38.6	5.0	155376	9	AC027026
c	57	38.6	5.0	231113	2	AC094980
c	58	38.6	5.0	241062	2	AC113725
c	59	38.2	5.0	849	1	AF405549
c	60	38.2	5.0	7218	6	I66494
c	61	38.2	5.0	89712	2	AC021459
c	62	38.2	5.0	171627	2	AC117776
c	63	38.2	5.0	192885	2	AC117732
c	64	38.2	5.0	195499	2	AC092257
c	65	38.2	5.0	243990	2	AC092260
c	66	38.2	5.0	258805	2	AC113467
c	67	38	5.0	185143	2	AC025861
c	68	38	5.0	216636	2	AC112069
c	69	38	5.0	244687	2	AC095483
c	70	37.8	4.9	151900	9	AC107419
c	71	37.8	4.9	154594	9	AL161722
c	72	37.8	4.9	167395	9	AC055858
c	73	37.8	4.9	169742	10	AL646101
c	74	37.8	4.9	214702	2	AC020689
c	75	37.8	4.9	226119	2	AC099445
c	76	37.8	4.9	228414	2	AC128563
c	77	37.8	4.9	231998	2	AC113222
c	78	37.6	4.9	104296	8	CNS08C8H
c	79	37.6	4.9	128945	8	AL449083
c	80	37.6	4.9	138586	8	AC144726
c	81	37.6	4.9	157677	2	AP002470
c	82	37.6	4.9	162646	9	AC078809
c	83	37.6	4.9	241783	2	AC106100
c	84	37.6	4.9	244861	2	AC106089
c	85	37.4	4.9	33991	9	AC125815
c	86	37.4	4.9	54255	8	AP003608
c	87	37.4	4.9	110000	1	CR543861_23
c	88	37.4	4.9	115768	2	AP000712
c	89	37.4	4.9	119300	9	AC125766
c	90	37.4	4.9	165990	2	AC093287
c	91	37.4	4.9	172697	9	AC055782
c	92	37.4	4.9	174616	10	AC109307

Continuation (2 of
BX935444 Gallus ga
AC135628 Homo sapi
AC116347 Homo sapi
AC140830 Homo sapi
AC145037 Homo sapi
AC145031 Homo sapi
AC145101 Homo sapi
AX083744 Sequence
AX655393 Sequence
BX649358 Zebrafish
AC068392 Homo sapi
AC108695 Homo sapi
AC097472 Homo sapi
AC023143 Homo sapi
AL121830 Human DNA
AC148196 Callithri
AC107484 Homo sapi
AC108075 Homo sapi
AC007682 Homo sapi
AC124845 Rattus no
AC129448 Rattus no
CQ719320 Sequence
Y16241 Homo sapien
AK098573 Homo sapi
AP002958 Homo sapi
AC011980 Homo sapi
AC079194 Homo sapi
AP001532 Homo sapi
AC090358 Homo sapi
AP001400 Homo sapi
BX247881 Zebrafish
BX927289 Danio rer
AC150601 Callithri
AX344563 Sequence
AC135551 Sus scrofa
AC027026 Homo sapi
AC094980 Rattus no
AC113725 Rattus no
AF405549 Helicobac
I66494 Sequence 14
AC021459 Homo sapi
AC117776 Mus muscu
AC117732 Mus muscu
AC092257 Mus muscu
AC092260 Mus muscu
AC113467 Mus muscu
AC025861 Homo sapi
AC112069 Rattus no
AC095483 Rattus no
AC107419 Homo sapi
AL161722 Human DNA
AC055858 Homo sapi
AL646101 Mouse DNA
AC020689 Homo sapi
AC099445 Rattus no
AC128563 Rattus no
AC113222 Homo sapi
AL731877 Oryza sat
AL449083 Human DNA
AC144726 Medicago
AP002470 Homo sapi
AC078809 Homo sapi
AC106100 Rattus no
AC106089 Rattus no
AC125815 Homo sapi
AP003608 Oryza sat
Continuation (24 o
AP000712 Homo sapi
AC125766 Homo sapi
AC093287 Homo sapi
AC055782 Homo sapi
AC109307 Mus muscu

93	37.4	4.9	181568	2	AC122124	AC122124 Mus muscu	166	36.2	4.7	1479	9	HSAL33356	AJL133356 Homo sapi
94	37.4	4.9	182816	5	AC145913	AC145913 Gallus ga	167	36.2	4.7	3274	6	BD193756	BD193756 Enterococ
95	37.4	4.9	187131	2	AP001535	AP001535 Homo sapi	168	36.2	4.7	3751	9	AF047368	AF047368 Homo sapi
96	37.4	4.9	187332	9	AC053544	AC053544 Homo sapi	169	36.2	4.7	70360	2	AC101122	AC101122 Mus muscu
C 97	37.4	4.9	205069	10	AC121778	AC121778 Mus muscu	170	36.2	4.7	110000	2	AC141455_2	Continuation (3 of
C 98	37.4	4.9	214795	2	AC110449	AC110449 Rattus no	171	36.2	4.7	139469	2	AC143350	AC143350 Homo sapi
C 99	37.4	4.9	217393	2	AP001122	AP001122 Homo sapi	172	36.2	4.7	150222	2	BX942815	BX942815 Danio rer
100	37.2	4.9	21335	5	AF287485	AF287485 Oncorhync	173	36.2	4.7	150296	9	HU091326	HU091326 Homo sapien
101	37.2	4.9	112484	10	AL954640	AL954640 Mouse DNA	174	36.2	4.7	153365	2	AC142443	AC142443 Homo sapi
C 102	37.2	4.9	127653	8	AC135316	AC135316 Medicago	175	36.2	4.7	154685	2	AC144355	AC144355 Homo sapi
103	37.2	4.9	129108	9	AC011482	AC011482 Homo sapi	176	36.2	4.7	158168	2	AC142544	AC142544 Homo sapi
104	37.2	4.9	147890	10	BX936292	BX936292 Mouse DNA	177	36.2	4.7	161136	2	AC142078	AC142078 Homo sapi
C 105	37.2	4.9	151950	2	AC084813	AC084813 Homo sapi	178	36.2	4.7	172367	2	AC024457	AC024457 Homo sapi
C 106	37.2	4.9	162525	5	BX004981	BX004981 Zebrafish	179	36.2	4.7	177962	10	AC147251	AC147251 Mus muscu
107	37.2	4.9	171061	2	BX950177	BX950177 Danio rer	180	36.2	4.7	180504	9	AL354793	AL354793 Human DNA
108	37.2	4.9	176010	5	AL935062	AL935062 Zebrafish	181	36.2	4.7	182402	2	AC116454	AC116454 Mus muscu
C 109	37.2	4.9	180106	10	AL731676	AL731676 Mouse DNA	182	36.2	4.7	183285	10	AC128665	AC128665 Mus muscu
C 110	37.2	4.9	181532	2	AC020700	AC020700 Homo sapi	183	36.2	4.7	190015	9	AL450342	AL450342 Human DNA
111	37.2	4.9	184213	9	AC073539	AC073539 Homo sapi	184	36.2	4.7	195808	2	AC142442	AC142442 Homo sapi
112	37.2	4.9	195634	2	AC150472	AC150472 Papio anu	185	36.2	4.7	196919	2	AC142542	AC142542 Homo sapi
C 113	37.2	4.9	209567	2	AC148249	AC148249 Otolomur	186	36.2	4.7	206624	9	AP001825	AP001825 Homo sapi
C 114	37	4.8	92320	9	AC024446	AC024446 Homo sapi	187	36.2	4.7	220804	10	AC091283	AC091283 Mus muscu
C 115	37	4.8	150181	5	BX248087	BX248087 Zebrafish	188	36.2	4.7	243754	2	AC146822	AC146822 Otolomur
C 116	37	4.8	157450	2	AC150735	AC150735 Papio anu	189	36.2	4.7	326434	1	AE016947	AE016947 Enterococ
C 117	37	4.8	185470	9	AC010947	AC010947 Homo sapi	190	36	4.7	3145	10	BC054395	BC054395 Mus muscu
C 118	37	4.8	194257	5	BX255948	BX255948 Zebrafish	191	36	4.7	5807	6	AX346056	AX346056 Sequence
C 119	37	4.8	231919	2	AC111770	AC111770 Rattus no	192	36	4.7	105087	9	AC093884	AC093884 Homo sapi
120	37	4.8	347050	3	FFA923351	AL929351 Plasmid	193	36	4.7	138603	2	AC034182	AC034182 Homo sapi
C 121	36.8	4.8	12540	1	AE008523	AE008523 Streptococ	194	36	4.7	139215	8	AC126780	AC126780 Medicago
C 122	36.8	4.8	122543	9	AC012470	AC012470 Homo sapi	195	36	4.7	162556	9	AC006017	AC006017 Homo sapi
C 123	36.8	4.8	124018	2	AC149732	AC149732 Bos tauru	196	36	4.7	170346	2	CR555298	CR555298 Danio rer
C 124	36.8	4.8	128561	2	AC068729	AC068729 Homo sapi	197	36	4.7	174902	2	AC110071	AC110071 Homo sapi
C 125	36.8	4.8	161661	2	AC119283	AC119283 Mus muscu	198	36	4.7	182658	2	AC135844	AC135844 Felis cat
C 126	36.8	4.8	166120	9	AC073588	AC073588 Homo sapi	199	36	4.7	193708	9	AC005035	AC005035 Homo sapi
C 127	36.8	4.8	184989	10	AC131652	AC131652 Mus muscu	200	36	4.7	331039	3	AC116979	AC116979 Dictyoste
C 128	36.8	4.8	199896	2	AC127812	AC127812 Rattus no	201	35.8	4.7	393	6	AR479582	AR479582 Sequence
C 129	36.8	4.8	219283	2	AC108550	AC108550 Rattus no	202	35.8	4.7	832	6	AX972010	AX972010 Sequence
C 130	36.8	4.8	231373	2	AC112543	AC112543 Rattus no	203	35.8	4.7	832	6	BD110729	BD110729 EST and e
C 131	36.8	4.8	252614	5	BX255907	BX255907 Zebrafish	204	35.8	4.7	65114	9	AL590225	AL590225 Human DNA
C 132	36.6	4.8	2755	14	AF014881	AF014881 Hollyhock	205	35.8	4.7	86798	2	AL133317	AL133317 Mus muscu
C 133	36.6	4.8	37425	3	U80842	U80842 Caenorhabdi	206	35.8	4.7	102552	9	HS46062	HS46062 Human DNA
C 134	36.6	4.8	97979	9	HS68868	AL445184 Human DNA	207	35.8	4.7	110000	8	CR380951_2	Continuation (3 of
C 135	36.6	4.8	116380	9	HS68868	AL031671 Human DNA	208	35.8	4.7	151792	10	AL365333	AL365333 Mouse DNA
C 136	36.6	4.8	132688	2	AC119878	AC119878 Mus muscu	209	35.8	4.7	162905	9	AL129318	AL129318 Mus muscu
C 137	36.6	4.8	133974	2	AC108894	AC108894 Bos tauru	210	35.8	4.7	173403	9	BS000114	BS000114 Pan trogl
C 138	36.6	4.8	135209	9	HS42616	AL020997 Human DNA	211	35.8	4.7	173403	10	AL773587	AL773587 Mouse DNA
C 139	36.6	4.8	149176	10	AC132097	AC132097 Mus muscu	212	35.8	4.7	175713	10	AC068949	AC068949 Homo sapi
C 140	36.6	4.8	150553	2	AC127261	AC127261 Mus muscu	213	35.8	4.7	178193	2	AC068949	AC068949 Homo sapi
C 141	36.6	4.8	150594	2	AC108889	AC108889 Bos tauru	214	35.8	4.7	182426	2	BX571738	BX571738 Danio rer
C 142	36.6	4.8	156233	10	AC119615	AC119615 Rattus no	215	35.8	4.7	186277	10	AC125154	AC125154 Mus muscu
C 143	36.6	4.8	166294	2	AC122113	AC122113 Atelerix	216	35.8	4.7	193386	10	AC117693	AC117693 Mus muscu
C 144	36.6	4.8	183856	2	AC021300	AC021300 Homo sapi	217	35.8	4.7	248276	2	AC103007	AC103007 Rattus no
C 145	36.6	4.8	193094	2	AC136129	AC136129 Rattus no	218	35.8	4.7	275820	2	AC112429	AC112429 Rattus no
C 146	36.6	4.8	202792	9	CNS06083	AL391158 Human chr	219	35.6	4.6	400	11	GI4360	GI4360 SHGC-8871 H
C 147	36.6	4.8	241948	2	AC115203	AC115203 Rattus no	220	35.6	4.6	10029	1	AE010608	AE010608 Fusobacte
C 148	36.6	4.8	257118	2	AC108341	AC108341 Rattus no	221	35.6	4.6	29255	8	SPCC777	AL031532 S.pombe c
C 149	36.6	4.8	289087	2	AC110678	AC110678 Rattus no	222	35.6	4.6	61475	2	AC100785	AC100785 Homo sapi
C 150	36.4	4.8	369	6	AR348554	AR348554 Sequence	223	35.6	4.6	71661	10	AL954643	AL954643 Mouse DNA
C 151	36.4	4.8	2145	3	DDISASIA	M34456 Dictyosteli	224	35.6	4.6	110000	2	AC096496_2	Continuation (3 of
C 152	36.4	4.8	41483	3	U80023	U80023 Caenorhabdi	225	35.6	4.6	126746	9	AC008840	AC008840 Human DNA s
C 153	36.4	4.8	84632	9	AL450026	AL450026 Human DNA	226	35.6	4.6	133120	9	HS393P23	295400 Homo sapi
C 154	36.4	4.8	100000	9	AP000070	AP000070 Homo sapi	227	35.6	4.6	160770	9	AC008511	AC008511 Homo sapi
C 155	36.4	4.8	100925	9	AC012627	AC012627 Homo sapi	228	35.6	4.6	162365	5	BX322622	BX322622 Zebrafish
C 156	36.4	4.8	156583	9	AP006304	AP006304 Homo sapi	229	35.6	4.6	167789	2	AC084260	AC084260 Homo sapi
C 157	36.4	4.8	176099	9	AC108201	AC108201 Homo sapi	230	35.6	4.6	167794	9	AC092472	AC092472 Homo sapi
C 158	36.4	4.8	183031	10	AC126795	AC126795 Mus muscu	231	35.6	4.6	170973	9	AC090097	AC090097 Homo sapi
C 159	36.4	4.8	188215	2	AC025725	AC025725 Caenorhab	232	35.6	4.6	182635	3	AC023729	AC023729 Drosophill
C 160	36.4	4.8	188616	3	AC084158	AC084158 Caenorhab	233	35.6	4.6	187230	3	AC023719	AC023719 Drosophill
C 161	36.4	4.8	206136	9	AC068037	AC068037 Homo sapi	234	35.6	4.6	219831	2	CR293498	CR293498 Danio rer
C 162	36.4	4.8	211750	9	AP006306	AP006306 Homo sapi	235	35.6	4.6	221189	2	AC131130	AC131130 Rattus no
C 163	36.4	4.8	239081	2	AC006892	AC006892 Caenorhab	236	35.6	4.6	236824	2	AC122632	AC122632 Rattus no
C 164	36.2	4.7	427	6	CQ455645	CQ455645 Sequence	237	35.6	4.6	241687	2	AC096392	AC096392 Rattus no
C 165	36.2	4.7	494	9	HUMMSP02	M34374 Homo sapien	238	35.6	4.6	255619	2	AC107503	AC107503 Rattus no

C 239	35.6	4.6	267991	2	AC112578	AC112578 Rattus no	C 312	35	4.6	171518	2	AL589697	AL589697 Homo sapi
C 240	35.6	4.6	270897	3	AE096415	AE096415 Rattus no	C 313	35	4.6	174347	10	AL928956	AL928956 Mouse DNA
C 241	35.6	4.6	290970	3	AE003446	AE003446 Drosophill	C 314	35	4.6	176508	9	AL365498	AL365498 Human DNA
C 242	35.4	4.6	1292	10	BC024451	BC024451 Mus muscu	C 315	35	4.6	177004	2	AC129114	AC129114 Rattus no
C 243	35.4	4.6	1512	10	BC016446	BC016446 Mus muscu	C 316	35	4.6	179085	9	AC011611	AC011611 Homo sapi
C 244	35.4	4.6	2723	1	BGR439506	AJ439506 Bartonell	C 317	35	4.6	183137	9	AC008734	AC008734 Homo sapi
C 245	35.4	4.6	2725	1	BGR422079	AJ422079 Bartonell	C 318	35	4.6	184809	9	BS000097	BS000097 Pan trogl
C 246	35.4	4.6	27743	3	L10990	L10990 Caenorhabdi	C 319	35	4.6	185276	2	AC136050	AC136050 Rattus no
C 247	35.4	4.6	103930	8	AY6323359	AY6323359 Goeypium	C 320	35	4.6	188858	9	AC090621	AC090621 Homo sapi
C 248	35.4	4.6	132505	2	AC015393	AC015393 Drosophill	C 321	35	4.6	189867	2	AC128902	AC128902 Rattus no
C 249	35.4	4.6	151348	9	AC015807	AC015807 Homo sapi	C 322	35	4.6	192390	2	AC102900	AC102900 Mus muscu
C 250	35.4	4.6	153496	2	AC087044	AC087044 Homo sapi	C 323	35	4.6	197431	9	AL360157	AL360157 Human DNA
C 251	35.4	4.6	153617	2	AC142616	AC142616 Macaca mu	C 324	35	4.6	201948	2	AC142435	AC142435 Rattus no
C 252	35.4	4.6	162630	2	AC147730	AC147730 Oryctolag	C 325	35	4.6	202392	2	AC021018	AC021018 Homo sapi
C 253	35.4	4.6	163453	9	AC099561	AC099561 Homo sapi	C 326	35	4.6	208281	2	AC106260	AC106260 Rattus no
C 254	35.4	4.6	172077	9	AC023514	AC023514 Homo sapi	C 327	35	4.6	211621	2	AC127128	AC127128 Rattus no
C 255	35.4	4.6	172367	2	AC024457	AC024457 Homo sapi	C 328	35	4.6	219228	2	AC123889	AC123889 Rattus no
C 256	35.4	4.6	172914	9	AP002791	AP002791 Homo sapi	C 329	35	4.6	220737	2	AC128459	AC128459 Rattus no
C 257	35.4	4.6	173230	2	AC012216	AC012216 Homo sapi	C 330	35	4.6	242885	2	AC097836	AC097836 Rattus no
C 258	35.4	4.6	175668	2	AC027268	AC027268 Homo sapi	C 331	35	4.6	250029	3	AE014820	AE014820 Plasmodiu
C 259	35.4	4.6	179856	3	AC010067	AC010067 Drosophill	C 332	35	4.6	258263	2	AC097043	AC097043 Rattus no
C 260	35.4	4.6	180222	9	AC009161	AC009161 Homo sapi	C 333	35	4.6	259902	2	AC102170	AC102170 Mus muscu
C 261	35.4	4.6	188379	9	AC026200	AC026200 Homo sapi	C 334	35	4.6	259967	2	AC105625	AC105625 Rattus no
C 262	35.4	4.6	193372	9	AC026217	AC026217 Homo sapi	C 335	35	4.6	265061	2	AC123375	AC123375 Rattus no
C 263	35.4	4.6	201531	9	AC026219	AC026219 Homo sapi	C 336	35	4.6	266766	2	AC094770	AC094770 Rattus no
C 264	35.4	4.6	222792	2	AC134359	AC134359 Rattus no	C 337	35	4.6	281307	2	AC106352	AC106352 Rattus no
C 265	35.4	4.6	223754	5	BX323557	BX323557 Zebrafish	C 338	35	4.6	299015	2	AC006842	AC006842 Caenorhab
C 266	35.4	4.6	317354	3	AE003478	AE003478 Drosophill	C 339	34.8	4.5	852	6	AX954037	AX954037 Sequence
C 267	35.2	4.6	10865	6	QO807288	QO807288 Sequence	C 340	34.8	4.5	870	6	AX953487	AX953487 Sequence
C 268	35.2	4.6	84876	9	BX284698	BX284698 Human DNA	C 341	34.8	4.5	1809	6	AR452918	AR452918 Sequence
C 269	35.2	4.6	103347	9	AL136086	AL136086 Human DNA	C 342	34.8	4.5	1809	6	AR452918	AR452918 Sequence
C 270	35.2	4.6	110000	2	AC106945	Continuation (3 of	C 343	34.8	4.5	1809	8	AF364866	AF364866 Helianthu
C 271	35.2	4.6	120787	8	AC002292	AC002292 Arabidops	C 344	34.8	4.5	5055	10	AF162282	AF162282 Mus muscu
C 272	35.2	4.6	132398	10	AC125278	AC125278 Rattus no	C 345	34.8	4.5	5249	10	BC053047	BC053047 Mus muscu
C 273	35.2	4.6	136532	2	AC139557	AC139557 Rattus no	C 346	34.8	4.5	5254	10	AF036007	AF036007 Mus muscu
C 274	35.2	4.6	138062	9	AL161938	AL161938 Human DNA	C 347	34.8	4.5	5261	10	BC048148	BC048148 Mus muscu
C 275	35.2	4.6	139109	8	AP005051	AP005051 Oryza sat	C 348	34.8	4.5	5267	10	MMDNAMET	X14805 Mus muscu
C 276	35.2	4.6	158574	2	AC024895	AC024895 Homo sapi	C 349	34.8	4.5	5543	10	AF175432	AF175432 Mus muscu
C 277	35.2	4.6	161816	10	AL773547	AL773547 Mouse DNA	C 350	34.8	4.5	5877	10	AF036009	AF036009 Mus muscu
C 278	35.2	4.6	164550	9	CNS01RHV	AL162633 Human chr	C 351	34.8	4.5	11130	1	AE009996	AE009996 Streptoco
C 279	35.2	4.6	170427	2	AC006095	AC006095 Homo sapi	C 352	34.8	4.5	11131	1	AE006511	AE006511 Streptoco
C 280	35.2	4.6	173067	9	AC026029	AC026029 Homo sapi	C 353	34.8	4.5	11334	3	CEY68A4A	AL021503 Caenorhab
C 281	35.2	4.6	173921	9	AC084759	AC084759 Homo sapi	C 354	34.8	4.5	34971	2	AC149340	AC149340 Phakopsor
C 282	35.2	4.6	175274	9	AP004286	AP004286 Homo sapi	C 355	34.8	4.5	50029	1	AE014144	AE014144 Streptoco
C 283	35.2	4.6	186183	9	AC026827	AC026827 Homo sapi	C 356	34.8	4.5	50466	2	AC136370	AC136370 Homo sapi
C 284	35.2	4.6	187051	2	AC122564	AC122564 Mus muscu	C 357	34.8	4.5	50466	2	AC136370	AC136370 Homo sapi
C 285	35.2	4.6	187051	9	AC011474	AC011474 Homo sapi	C 358	34.8	4.5	57180	8	ATF18D22	AL360334 Arabidops
C 286	35.2	4.6	195234	2	AC141878	AC141878 Mus muscu	C 359	34.8	4.5	63939	9	AL359200	AL359200 Human DNA
C 287	35.2	4.6	196085	2	AC025971	AC025971 Homo sapi	C 360	34.8	4.5	70805	8	AP006129	AP006129 Lotus cor
C 288	35.2	4.6	197650	2	AC027690	AC027690 Homo sapi	C 361	34.8	4.5	77567	8	ATT19F6	AL109619 Arabidops
C 289	35.2	4.6	198278	2	AC010097	AC010097 Homo sapi	C 362	34.8	4.5	90246	2	AC022686	AC022686 Homo sapi
C 290	35.2	4.6	204524	2	AC055796	AC055796 Homo sapi	C 363	34.8	4.5	94125	9	AC016966	AC016966 Homo sapi
C 291	35.2	4.6	223182	5	AL929049	AL929049 Zebrafish	C 364	34.8	4.5	97711	8	ATT16K5	AL132965 Arabidops
C 292	35.2	4.6	230701	2	AC096135	AC096135 Rattus no	C 365	34.8	4.5	98505	8	AP006692	AP006692 Lotus cor
C 293	35.2	4.6	247544	2	AC092741	AC092741 Mus muscu	C 366	34.8	4.5	109043	5	CNS08CA7	AL048032 BAC 30B15
C 294	35.2	4.6	253140	2	AC094055	AC094055 Rattus no	C 367	34.8	4.5	109398	9	AC044817	AC044817 Homo sapi
C 295	35.2	4.6	254575	2	AC127999	AC127999 Rattus no	C 368	34.8	4.5	110000	1	CP000003	Continuation (5 of
C 296	35.2	4.6	269273	2	AC096095	AC096095 Rattus no	C 369	34.8	4.5	11656	8	ATAC002343	AC002343 Arabidops
C 297	35.2	4.6	315079	1	MPULM03	AL445565 Mycoplaem	C 370	34.8	4.5	127501	2	AL357852	AL357852 Homo sapi
C 298	35.2	4.6	343882	2	AC114375	AC114375 Rattus no	C 371	34.8	4.5	131286	4	AB053451	AB053451 Sus scrofa
C 299	35	4.6	509	11	BV012226	BV012226 MASC STS1	C 372	34.8	4.5	139378	9	HS64K7	AL031668 Human DNA
C 300	35	4.6	596	11	BV012227	BV012227 MASC STS1	C 373	34.8	4.5	143687	9	AC136793	AC136793 Homo sapi
C 301	35	4.6	794	5	AY522638	AY522638 Oreochrom	C 374	34.8	4.5	154137	2	AC139735	AC139735 Canis fam
C 302	35	4.6	1627	8	AY102636	AY102636 Arabidops	C 375	34.8	4.5	154326	2	AC137907	AC137907 Canis fam
C 303	35	4.6	2181	1	CACSPD	Z50009 C.acetobuty	C 376	34.8	4.5	156630	9	BS000087	BS000087 Pan trogl
C 304	35	4.6	2755	14	AY036009	AY036009 Hollyhock	C 377	34.8	4.5	160676	2	AC022920	AC022920 Homo sapi
C 305	35	4.6	42434	3	AF045641	AF045641 Caenorhab	C 378	34.8	4.5	162087	2	AC011576	AC011576 Homo sapi
C 306	35	4.6	68790	9	HSJ287H17	AL121970 Human DNA	C 379	34.8	4.5	165333	2	CR626869	CR626869 Danio rer
C 307	35	4.6	86436	8	AC007323	AC007323 Genomic s	C 380	34.8	4.5	168311	2	AC087788	AC087788 Homo sapi
C 308	35	4.6	104364	8	AC006919	AC006919 Arabidops	C 381	34.8	4.5	168366	2	AC069409	AC069409 Homo sapi
C 309	35	4.6	117189	2	AC147547	AC147547 Rattus no	C 382	34.8	4.5	168843	9	AC068207	AC068207 Homo sapi
C 310	35	4.6	156134	2	BX927097	BX927097 Danio rer	C 383	34.8	4.5	169637	9	AC113412	AC113412 Homo sapi
C 311	35	4.6	169207	10	AC119813	AC119813 Mus muscu	C 384	34.8	4.5	169964	9	AC055710	AC055710 Homo sapi

C 385	34.8	4.5	171545	9	AC008394	AC008394 Homo sapi	C 458	34.4	4.5	2711	10	BC005616	BC005616 Mus muscu
386	34.8	4.5	171899	2	AC020562	AC020562 Homo sapi	459	34.4	4.5	32428	10	AF285839	AF285839 Mus muscu
C 387	34.8	4.5	172650	2	AC040920	AC040920 Homo sapi	460	34.4	4.5	60554	2	AC101366	AC101366 Mus muscu
C 388	34.8	4.5	174226	9	AC093847	AC093847 Homo sapi	461	34.4	4.5	74269	2	AC136368	AC136368 Homo sapi
389	34.8	4.5	176512	9	AC012323	AC012323 Homo sapi	462	34.4	4.5	84122	2	AL133463	AL133463 Human DNA
C 390	34.8	4.5	176681	5	BX005052	BX005052 Zebrafish	C 463	34.4	4.5	85693	2	AC124117	AC124117 Mus muscu
391	34.8	4.5	177770	9	AC110027	AC110027 Homo sapi	C 464	34.4	4.5	88619	9	AC097723	AC097723 Homo sapi
392	34.8	4.5	177872	10	AC093371	AC093371 Genomic s	465	34.4	4.5	96726	2	HS1178F13	HS1178F13 Homo sapi
393	34.8	4.5	180606	2	AC073406	AC073406 Homo sapi	466	34.4	4.5	102842	10	AL671903	AL671903 Mouse DNA
394	34.8	4.5	180684	9	AC135626	AC135626 Homo sapi	467	34.4	4.5	125020	9	AF429315	AF429315 Homo sapi
C 395	34.8	4.5	191988	2	AC135980	AC135980 Homo sapi	C 468	34.4	4.5	128000	2	AC004046	AC004046 Homo sapi
396	34.8	4.5	196677	8	ATCHR1V60	AL161560 Arabidops	C 469	34.4	4.5	139131	2	AP004385	AP004385 Oryza sat
C 397	34.8	4.5	197864	9	HSY214H10	AL022344 Human DNA	470	34.4	4.5	143756	9	AC136365	AC136365 Homo sapi
C 398	34.8	4.5	205642	2	AC007898	AC007898 Homo sapi	C 471	34.4	4.5	149577	9	AP005902	AP005902 Homo sapi
C 399	34.8	4.5	205831	2	AC074192	AC074192 Homo sapi	C 472	34.4	4.5	150399	9	AC093680	AC093680 Homo sapi
400	34.8	4.5	206852	9	AC091182	AC091182 Homo sapi	C 473	34.4	4.5	152324	2	CR136938	CR136938 Homo sapi
401	34.8	4.5	211005	2	AC118299	AC118299 Rattus no	474	34.4	4.5	154675	2	CR354440	CR354440 Danio rer
402	34.8	4.5	214303	2	AC124993	AC124993 Mus muscu	475	34.4	4.5	156612	2	AC147212	AC147212 Pan trogl
403	34.8	4.5	226067	2	AC138358	AC138358 Mus muscu	476	34.4	4.5	156902	2	AC073630	AC073630 Homo sapi
C 404	34.8	4.5	241629	2	AC107491	AC107491 Rattus no	C 477	34.4	4.5	164363	2	AC073229	AC073229 Homo sapi
C 405	34.8	4.5	243065	2	AC112818	AC112818 Rattus no	C 478	34.4	4.5	164688	2	AC138727	AC138727 Pongo pyg
406	34.8	4.5	243072	6	AX770904	AX770904 Sequence	479	34.4	4.5	168117	10	AC132352	AC132352 Mus muscu
C 407	34.8	4.5	249995	3	AE014840	AE014840 Plasmodiu	480	34.4	4.5	188278	10	AC126246	AC126246 Mus muscu
408	34.8	4.5	252161	2	AC129382	AC129382 Rattus no	C 481	34.4	4.5	189453	9	AC096558	AC096558 Homo sapi
C 409	34.8	4.5	262852	2	AC096331	AC096331 Rattus no	C 482	34.4	4.5	172265	2	CR376845	CR376845 Danio rer
410	34.8	4.5	282915	2	AC098165	AC098165 Rattus no	483	34.4	4.5	172695	9	AC068303	AC068303 Homo sapi
C 411	34.8	4.5	325650	1	AP005145	AP005145 Streptoco	484	34.4	4.5	173357	9	AC113145	AC113145 Homo sapi
C 412	34.8	4.5	349318	1	BX571863	BX571863 Phototrab	C 485	34.4	4.5	175952	8	AC069285	AC069285 Homo sapi
413	34.6	4.5	6981	5	DYGCCAIB	LI2532 Discozyme o	C 486	34.4	4.5	176293	2	AP005158	AP005158 Oryza sat
C 414	34.6	4.5	16545	6	AX344953	AX344953 Sequence	C 487	34.4	4.5	177537	2	CR407599	CR407599 Danio rer
C 415	34.6	4.5	46778	9	AL451083	AL451083 Human DNA	C 488	34.4	4.5	178752	9	AC021889	AC021889 Homo sapi
C 416	34.6	4.5	98078	9	AL451083	AL451083 Human DNA	489	34.4	4.5	180424	9	AC106860	AC106860 Homo sapi
417	34.6	4.5	99592	9	AF263284	AF263284 Homo sapi	C 490	34.4	4.5	180588	5	AL954672	AL954672 Zebrafish
C 418	34.6	4.5	104630	9	AC007848	AC007848 Homo sapi	491	34.4	4.5	182178	9	AL138711	AL138711 Human DNA
C 419	34.6	4.5	106434	8	AP004847	AP004847 Oryza sat	492	34.4	4.5	185161	2	AC116732	AC116732 Mus muscu
C 420	34.6	4.5	122404	2	AC136155	AC136155 Rattus no	C 493	34.4	4.5	191265	2	AC068996	AC068996 Homo sapi
C 421	34.6	4.5	128861	5	BX294435	BX294435 Zebrafish	494	34.4	4.5	191373	9	AC017067	AC017067 Homo sapi
C 422	34.6	4.5	150295	5	BX005103	BX005103 Zebrafish	C 495	34.4	4.5	192638	2	AC101861	AC101861 Mus muscu
C 423	34.6	4.5	154256	5	BX511192	BX511192 Zebrafish	C 496	34.4	4.5	194337	2	AC117948	AC117948 Homo sapi
424	34.6	4.5	155378	2	AC023536	AC023536 Homo sapi	497	34.4	4.5	195408	2	AC109270	AC109270 Mus muscu
C 425	34.6	4.5	156150	2	CR524827	CR524827 Danio rer	C 498	34.4	4.5	196356	10	AC102637	AC102637 Mus muscu
C 426	34.6	4.5	158255	2	AC025695	AC025695 Homo sapi	499	34.4	4.5	196566	10	AL663045	AL663045 Mouse DNA
C 427	34.6	4.5	160295	10	AC122884	AC122884 Mus muscu	500	34.4	4.5	197775	9	AC012366	AC012366 Homo sapi
C 428	34.6	4.5	162472	9	CNS01DUW	AL133371 Human chr	501	34.4	4.5	201307	2	AC141181	AC141181 Rattus no
C 429	34.6	4.5	166000	9	AL390731	AL390731 Human DNA	C 502	34.4	4.5	203626	2	AC138730	AC138730 Pongo pyg
C 430	34.6	4.5	168247	9	AC005014	AC005014 Homo sapi	C 503	34.4	4.5	203715	2	AC018807	AC018807 Homo sapi
C 431	34.6	4.5	168571	9	CNS01DUF	AL133249 BAC sequ	504	34.4	4.5	213387	2	AC109275	AC109275 Mus muscu
C 432	34.6	4.5	169010	10	AL672260	AL672260 Mouse DNA	505	34.4	4.5	213857	2	AC126310	AC126310 Rattus no
C 433	34.6	4.5	169720	2	AC024458	AC024458 Homo sapi	C 506	34.4	4.5	215553	2	AC092716	AC092716 Mus muscu
434	34.6	4.5	171490	2	AC022481	AC022481 Homo sapi	C 507	34.4	4.5	229829	2	AC055749	AC055749 Homo sapi
C 435	34.6	4.5	171747	10	AC132412	AC132412 Mus muscu	508	34.4	4.5	231239	2	AC133164	AC133164 Mus muscu
C 436	34.6	4.5	174801	9	AL445238	AL445238 Human DNA	C 509	34.4	4.5	235867	2	AC140226	AC140226 Mus muscu
C 437	34.6	4.5	175151	9	AL160152	AL160152 Human DNA	C 510	34.4	4.5	244678	2	AC127664	AC127664 Rattus no
438	34.6	4.5	176155	2	AC020879	AC020879 Mus muscu	C 511	34.4	4.5	248015	2	AC127748	AC127748 Rattus no
C 439	34.6	4.5	176724	2	AL359772	AL359772 Homo sapi	512	34.4	4.5	248164	2	AC096228	AC096228 Rattus no
C 440	34.6	4.5	179068	10	AL627125	AL627125 Mouse DNA	C 513	34.4	4.5	250029	3	AE014838	AE014838 Plasmodiu
441	34.6	4.5	181850	9	AC018680	AC018680 Homo sapi	514	34.4	4.5	251086	2	AC099142	AC099142 Rattus no
C 442	34.6	4.5	182703	2	AC073117	AC073117 Homo sapi	C 515	34.4	4.5	251932	2	AC120488	AC120488 Rattus no
443	34.6	4.5	187204	9	AC084082	AC084082 Homo sapi	C 516	34.2	4.5	1393	1	AF522261	AF522261 Haemophil
444	34.6	4.5	190585	2	AC109303	AC109303 Mus muscu	C 517	34.2	4.5	1477	1	AF522260	AF522260 Haemophil
445	34.6	4.5	192800	2	AC113288	AC113288 Mus muscu	C 518	34.2	4.5	1477	1	HIIGA66	HIIGA66 H.influenza
C 446	34.6	4.5	233118	2	AC140327	AC140327 Mus muscu	519	34.2	4.5	2153	5	AF287486	AF287486 Oncorhync
447	34.6	4.5	235412	2	AC106607	AC106607 Rattus no	520	34.2	4.5	2155	5	AF115521	AF115521 Oncorhync
448	34.6	4.5	237831	2	AC113715	AC113715 Rattus no	C 521	34.2	4.5	2607	3	AY345039	AY345039 Alodia ba
C 449	34.6	4.5	242118	2	AC106908	AC106908 Rattus no	522	34.2	4.5	16710	8	AY459338	AY459338 Oryza sat
450	34.6	4.5	245424	2	AC112822	AC112822 Rattus no	523	34.2	4.5	26498	1	AE000792	AE000792 Borrelia
C 451	34.6	4.5	278946	2	AC115321	AC115321 Rattus no	524	34.2	4.5	27999	8	SECC70	SECC70 S.pombe
452	34.6	4.5	295639	2	AL360019	AL360019 Homo sapi	C 525	34.2	4.5	58789	2	AC131580	AC131580 Mus muscu
C 453	34.6	4.5	325076	2	AC125912	AC125912 Rattus no	C 526	34.2	4.5	64512	9	AP000255	AP000255 Homo sapi
C 454	34.6	4.5	346970	2	BX510643	BX510643 Danio rer	527	34.2	4.5	64672	2	AC100019	AC100019 Mus muscu
C 455	34.4	4.5	734	14	AY556458	AY556458 Thielavio	528	34.2	4.5	76089	2	AC124285	AC124285 Homo sapi
C 456	34.4	4.5	1413	6	AX489469	AX489469 Sequence	C 529	34.2	4.5	83848	10	AF246978	AF246978 Mus muscu
457	34.4	4.5	1798	5	BC073257	BC073257 Xenopus 1	C 530	34.2	4.5	85268	2	AC022648	AC022648 Homo sapi

531	34.2	4.5	90551	10	AL928543	Mouse DNA
C 532	34.2	4.5	100000	9	AP000213	Homo sapi
C 533	34.2	4.5	110000	2	Continuation (3 of	
C 534	34.2	4.5	110000	6	AR406002_4	Continuation (5 of
535	34.2	4.5	117542	4	AC023193	Mus muscu
536	34.2	4.5	120016	8	AP004929	Lotus cor
C 537	34.2	4.5	126470	8	AL390234	Human DNA
C 538	34.2	4.5	132585	9	AC131947	Homo sapi
539	34.2	4.5	136653	9	AC026776	Homo sapi
540	34.2	4.5	136653	9	AC090111	Homo sapi
C 541	34.2	4.5	138338	9	AC146073	Pan trogl
C 542	34.2	4.5	147420	2	AC116850	Mus muscu
543	34.2	4.5	147715	9	AC022534	Homo sapi
C 544	34.2	4.5	147733	2	AC101914	Homo sapi
C 545	34.2	4.5	149298	9	AP000031	Mus muscu
C 546	34.2	4.5	160004	9	AL393118	Human DNA
C 547	34.2	4.5	162150	9	AC093877	Homo sapi
548	34.2	4.5	163566	4	AC139340	Atelerix
549	34.2	4.5	167364	10	AC121590	Mus muscu
550	34.2	4.5	168725	2	AC134536	Mus muscu
551	34.2	4.5	173492	2	AC111329	Rattus no
552	34.2	4.5	174092	2	AC069129	Homo sapi
553	34.2	4.5	174311	9	AC016816	Homo sapi
C 554	34.2	4.5	175467	2	AC079215	Homo sapi
C 555	34.2	4.5	176051	9	AC022008	Homo sapi
556	34.2	4.5	177034	8	CNS08CAC	Oryza sat
C 557	34.2	4.5	179200	2	AC134838	Mus muscu
558	34.2	4.5	180404	2	AC102167	Mus muscu
C 559	34.2	4.5	181557	10	AC069014	Mus muscu
560	34.2	4.5	181683	10	AC122180	Mus muscu
561	34.2	4.5	182228	9	AC036145	Mus muscu
562	34.2	4.5	183101	9	AC021915	Homo sapi
563	34.2	4.5	184738	9	AL162574	Human DNA
564	34.2	4.5	184794	5	AL929229	Zebrafish
C 565	34.2	4.5	185277	10	AC098567	Genomic s
C 566	34.2	4.5	186014	5	BX908749	Zebrafish
C 567	34.2	4.5	186296	2	AC117907	Rattus no
C 568	34.2	4.5	186719	2	CR628370	Danio rer
569	34.2	4.5	188891	2	AC021156	Homo sapi
570	34.2	4.5	190379	2	AC022386	Homo sapi
C 571	34.2	4.5	190630	9	AC117470	Homo sapi
572	34.2	4.5	190927	2	AC141748	Apis mell
573	34.2	4.5	193188	9	AC092140	Homo sapi
574	34.2	4.5	193892	2	AC073037	Homo sapi
C 575	34.2	4.5	194815	9	CNS01DVZ	Human chr
C 576	34.2	4.5	195211	2	CR352256	Danio rer
577	34.2	4.5	195425	10	AC125399	Mus muscu
578	34.2	4.5	195667	10	AC073918	Rattus no
579	34.2	4.5	200222	2	AC023555	Homo sapi
580	34.2	4.5	206075	2	AC120361	Mus muscu
C 581	34.2	4.5	207960	10	AC124173	Mus muscu
C 582	34.2	4.5	211668	2	AC115146	Rattus no
C 583	34.2	4.5	216217	10	AC107231	Mus muscu
C 584	34.2	4.5	218866	2	BX323890	Mus muscu
585	34.2	4.5	225514	2	AC024142	Mus muscu
C 586	34.2	4.5	226711	2	AC127440	Rattus no
587	34.2	4.5	227753	2	AC102131	Mus muscu
C 588	34.2	4.5	231382	2	AC095549	Rattus no
C 589	34.2	4.5	233358	2	AC095317	Rattus no
590	34.2	4.5	239847	10	AL591466	Mouse DNA
C 591	34.2	4.5	246688	2	AC112282	Rattus no
C 592	34.2	4.5	253751	2	AC051621	Mus muscu
593	34.2	4.5	256381	2	AC013610	Homo sapi
594	34.2	4.5	278521	2	AC092715	Homo sapi
C 595	34.2	4.5	340000	9	AP001712	Homo sapi
C 596	34.2	4.5	349980	6	AX696302	Sequence
597	34	4.4	1283	3	AF132555	Drosophila
598	34	4.4	1599	8	AK065805	Oryza sat
599	34	4.4	2918	8	AK103210	Oryza sat
C 600	34	4.4	4843	2	AC014531	Drosophila
C 601	34	4.4	5791	10	MM065403	Mus muscu
C 602	34	4.4	24142	6	AX537050	Sequence
603	34	4.4	43801	3	U28740	Caenorhabdi

C 604	34	4.4	59818	4	AC123367	
605	34	4.4	60962	2	AC103742	
C 606	34	4.4	79459	3	AC089995	
C 607	34	4.4	103196	3	AC023738	
C 608	34	4.4	110000	8	CR382136_03	
609	34	4.4	110000	8	CR382137_00	
C 610	34	4.4	110000	8	AY506529_0	
C 611	34	4.4	120583	8	OSJN00125	
612	34	4.4	134482	2	AC109786	
613	34	4.4	141009	2	AC109915	
C 614	34	4.4	142607	2	AC113578	
C 615	34	4.4	143153	2	AC025027	
616	34	4.4	144807	2	AC147413	
C 617	34	4.4	145766	8	OSJN00287	
C 618	34	4.4	149904	9	CNS01DSV	
C 619	34	4.4	150864	8	OSJN00053	
620	34	4.4	150892	4	AL929190	
621	34	4.4	152217	5	BX005104	
622	34	4.4	152776	2	BX897743	
623	34	4.4	152829	9	AC078793	
C 624	34	4.4	153607	2	AL355523	
C 625	34	4.4	154348	4	AC129961	
626	34	4.4	157176	9	AC007092	
C 627	34	4.4	158498	8	OSJN00300	
C 628	34	4.4	158504	2	AC107810	
629	34	4.4	158861	10	AL845273	
C 630	34	4.4	159422	2	CR391981	
C 631	34	4.4	160461	2	AC125270	
C 632	34	4.4	161514	10	BX004793	
633	34	4.4	162633	2	AC148483	
C 634	34	4.4	166989	8	AP005836	
C 635	34	4.4	167148	5	BX0088714	
636	34	4.4	167663	9	AC093854	
637	34	4.4	167778	2	AC132618	
C 638	34	4.4	173413	2	AC145309	
C 639	34	4.4	177248	5	AL329093	
640	34	4.4	182025	9	AL138900	
641	34	4.4	182144	9	AC009223	
C 642	34	4.4	182820	10	AC122446	
C 643	34	4.4	183092	5	AC145912	
C 644	34	4.4	187144	2	BX957353	
645	34	4.4	187674	2	AC013748	
646	34	4.4	189538	10	AP0116787	
647	34	4.4	193091	8	AP005508	
648	34	4.4	195068	10	AC019153	
649	34	4.4	196053	10	AC117684	
C 650	34	4.4	197109	10	AC122239	
651	34	4.4	197611	9	AL390840	
652	34	4.4	197859	2	AC137159	
C 653	34	4.4	198445	2	BX927295	
C 654	34	4.4	198523	10	AL845158	
655	34	4.4	199844	5	AL929319	
C 656	34	4.4	199912	2	AC141558	
657	34	4.4	200000	9	AB019440	
C 658	34	4.4	201299	9	AC007158	
C 659	34	4.4	203257	5	BX000993	
C 660	34	4.4	206524	2	AC141649	
C 661	34	4.4	209058	2	AC109267	
C 662	34	4.4	212485	10	AC090122	
663	34	4.4	215399	2	AC116268	
C 664	34	4.4	220430	2	AC095315	
665	34	4.4	226762	2	AC128126	
C 666	34	4.4	227353	2	AC141259	
C 667	34	4.4	230392	9	AC026672	
668	34	4.4	231589	2	AC118944	
C 669	34	4.4	234053	2	AC128262	
C 670	34	4.4	236013	2	AC106499	
C 671	34	4.4	240079	2	AC128364	
672	34	4.4	243782	2	BX548019	
673	34	4.4	246893	2	AC132513	
674	34	4.4	252480	2	AC103661	
C 675	34	4.4	256703	2	AC114076	
C 676	34	4.4	257816	2	AC131814	

AC123967	Sminthops
AC103742	Homo sapi
AC089995	Caenorhab
AC023738	Drosophila
Continuation (4 of	
CR382137	Debaromy
AY506529	zea maye
AL606938	Oryza sat
AC109786	Bos tauru
AC109915	Bos tauru
AC113578	Tetraodon
AC025027	Homo sapi
AC147413	Homo sapi
AL731644	Oryza sat
AL122020	Human chr
AL606623	Oryza sat
AL929190	Zebrafish
BX005104	Zebrafish
BX897743	Danio rer
AC078793	Homo sapi
AL355523	Homo sapi
AC129961	Sus scrofa
AC007092	Homo sapi
BX842603	Oryza sat
AC107810	Mus muscu
CR391981	Danio rer
AC125270	Mus muscu
BX004793	Mouse DNA
AC148483	Medicago
AP005836	Oryza sat
BX0088714	Zebrafish
AC093854	Homo sapi
AC132618	Mus muscu
AC145309	Homo sapi
AL929093	Zebrafish
AL389000	Human DNA
AC009223	Homo sapi
AC122446	Mus muscu
AC145912	Gallus ga
BX957353	Danio rer
AC013748	Homo sapi
AP0116787	Mus muscu
AP005508	Oryza sat
AC019153	Mus muscu
AC117684	Mus muscu
AC122239	Mus muscu
AL390840	Human DNA
AC137159	Rattus no
BX927295	Danio rer
AL845158	Mouse DNA
AL929319	Zebrafish
AC141558	Mus muscu
AB019440	Homo sapi
AC007158	Homo sapi
BX000993	Zebrafish
AC141649	Rattus no
AC109267	Mus muscu
AC090122	Mus muscu
AC116268	Rattus no
AC095315	Rattus no
AC128126	Rattus no
AC141259	Homo sapi
AC026672	Homo sapi
AC118944	Rattus no
AC128262	Rattus no
AC106499	Rattus no
AC128364	Rattus no
BX548019	Danio rer
AC132513	Rattus no
AC103661	Mus muscu
AC114076	Rattus no
AC131814	Rattus no

823	33.6	4.4	143107	9	AC005949	AC005949 Homo sapi	896	33.4	4.4	10001	6	CQ807313	CQ807313 Sequence
824	33.6	4.4	143549	2	AP003910	AL092910 Oryza sat	C 897	33.4	4.4	11049	1	AE006530	AE006530 Streptococ
825	33.6	4.4	145652	10	AL929262	AL929262 Mouse DNA	C 898	33.4	4.4	14186	5	XBUT15KB	Z54313 X.boreal
C 826	33.6	4.4	148900	2	AC025404	AC025404 Homo sapi	C 899	33.4	4.4	16967	3	AB055624	AB055624 Inverse
827	33.6	4.4	151046	8	AP004566	AP004566 Oryza sat	C 900	33.4	4.4	17308	10	AL929285	AL929285 Mouse DNA
828	33.6	4.4	151162	2	AC025601	AC025601 Homo sapi	C 901	33.4	4.4	23907	3	U61951	U61951 Caenorhabdi
829	33.6	4.4	154084	2	AC022311	AC022311 Homo sapi	C 902	33.4	4.4	34990	2	AC022112	AC022112 Homo sapi
830	33.6	4.4	154284	10	AC005992	AC005992 Mus muscu	C 903	33.4	4.4	38740	9	HSU59962	HSU59962 Human cosm
831	33.6	4.4	157000	2	AC026511	AC026511 Homo sapi	C 904	33.4	4.4	40600	3	CFP20D1	Z78542 Caenorhabdi
832	33.6	4.4	161633	2	AL592288	AL592288 Homo sapi	C 905	33.4	4.4	41618	9	AL355473	AL355473 Human DNA
833	33.6	4.4	161815	2	AC092015	AC092015 Homo sapi	C 906	33.4	4.4	51719	1	AE014147	AE014147 Streptococ
C 834	33.6	4.4	167758	2	AC068746	AC068746 Homo sapi	C 907	33.4	4.4	58366	6	AX647879	AX647879 Sequence
835	33.6	4.4	168672	2	AC024920	AC024920 Homo sapi	C 908	33.4	4.4	65521	2	AC101449	AC101449 Mus muscu
836	33.6	4.4	169557	9	AC024706	AC024706 Homo sapi	C 909	33.4	4.4	71953	8	AB081587	AB081587 Prunus du
837	33.6	4.4	170849	9	AC126366	AC126366 Homo sapi	C 910	33.4	4.4	79834	9	AP000948	AP000948 Homo sapi
838	33.6	4.4	171451	2	AC064838	AC064838 Homo sapi	C 911	33.4	4.4	81699	10	AL713925	AL713925 Mouse DNA
C 839	33.6	4.4	173308	9	HS859D4	AL035668 Human DNA	C 912	33.4	4.4	93301	2	AC074165	AC074165 Mus muscu
840	33.6	4.4	178975	2	AC109974	AC109974 Rattus no	C 913	33.4	4.4	97805	2	AC074157	AC074157 Mus muscu
841	33.6	4.4	179350	9	AC026351	AC026351 Homo sapi	C 914	33.4	4.4	97805	2	AC074157	AC074157 Mus muscu
C 842	33.6	4.4	179503	9	AL445468	AL445468 Human DNA	C 915	33.4	4.4	102375	2	AC025042	AC025042 Homo sapi
C 843	33.6	4.4	181433	9	CNS00006	AL049775 Human chr	C 916	33.4	4.4	105736	10	AL772359	AL772359 Mouse DNA
C 844	33.6	4.4	181527	10	AC140788	AC140788 Mus muscu	C 917	33.4	4.4	108112	5	BX470170	BX470170 Zebrafish
C 845	33.6	4.4	182207	2	AC109242	AC109242 Mus muscu	C 918	33.4	4.4	108189	9	AC007128	AC007128 Homo sapi
C 846	33.6	4.4	182934	5	EX000690	EX000690 Zebrafish	C 919	33.4	4.4	110000	1	CP000003_06	Continuation (7 of
C 847	33.6	4.4	190842	9	AC004885	AC004885 Homo sapi	C 920	33.4	4.4	110000	2	AC109620_0	AC109620 Mus muscu
C 848	33.6	4.4	191947	9	AC107016	AC107016 Homo sapi	C 921	33.4	4.4	110000	2	BX294172_1	Continuation (2 of
C 849	33.6	4.4	194770	2	AC149064	AC149064 Mus muscu	C 922	33.4	4.4	112070	9	AC068798	AC068798 Homo sapi
C 850	33.6	4.4	195921	8	ATCHRIV81	AL161585 Arabidops	C 923	33.4	4.4	113937	8	AC143338	AC143338 Medicago
851	33.6	4.4	197964	9	AC079904	AC079904 Homo sapi	C 924	33.4	4.4	115040	8	AC124954	AC124954 Medicago
852	33.6	4.4	198564	9	AC008581	AC008581 Homo sapi	C 925	33.4	4.4	123988	9	HSU914M10	AL121763 Human DNA
C 853	33.6	4.4	200097	2	AC129104	AC129104 Homo sapi	C 926	33.4	4.4	124964	9	AL159154	AL159154 Human DNA
854	33.6	4.4	202815	9	AF267169	AF267169 Homo sapi	C 927	33.4	4.4	138257	2	AC149471	AC149471 Medicago
855	33.6	4.4	207346	10	AC123608	AC123608 Mus muscu	C 928	33.4	4.4	138627	9	AC099500	AC099500 Homo sapi
856	33.6	4.4	207699	10	BX255938	BX255938 Mouse DNA	C 929	33.4	4.4	143092	2	AC051641	AC051641 Homo sapi
C 857	33.6	4.4	207699	2	BX470159	BX470159 Danio rer	C 930	33.4	4.4	147874	2	AC011278	AC011278 Homo sapi
C 858	33.6	4.4	209196	2	AC017024	AC017024 Homo sapi	C 931	33.4	4.4	149848	2	AC119516	AC119516 Rattus no
C 859	33.6	4.4	211296	10	AC113059	AC113059 Mus muscu	C 932	33.4	4.4	150438	9	AC099517	AC099517 Homo sapi
C 860	33.6	4.4	213223	2	CR376855	CR376855 Danio rer	C 933	33.4	4.4	151225	2	AC012625	AC012625 Homo sapi
C 861	33.6	4.4	216726	2	AC097270	AC097270 Pan trogl	C 934	33.4	4.4	156492	2	AC008460	AC008460 Homo sapi
C 862	33.6	4.4	221537	2	AC117664	AC117664 Mus muscu	C 935	33.4	4.4	158907	9	AC011890	AC011890 Homo sapi
C 863	33.6	4.4	236761	2	AC103282	AC103282 Rattus no	C 936	33.4	4.4	160558	2	AC025832	AC025832 Homo sapi
C 864	33.6	4.4	237468	2	AC108532	AC108532 Rattus no	C 937	33.4	4.4	160708	2	AC011962	AC011962 Homo sapi
865	33.6	4.4	241956	2	BX323993	BX323993 Mus muscu	C 938	33.4	4.4	162417	10	AC102769	AC102769 Mus muscu
866	33.6	4.4	243329	5	AC145979	AC145979 Gallus ga	C 939	33.4	4.4	163823	9	AC097372	AC097372 Homo sapi
C 867	33.6	4.4	246612	2	AC008579	AC008579 Homo sapi	C 940	33.4	4.4	164647	9	AC080183	AC080183 Homo sapi
C 868	33.6	4.4	246890	2	AC117302	AC117302 Rattus no	C 941	33.4	4.4	165965	2	AC012287	AC012287 Homo sapi
C 869	33.6	4.4	250096	10	AC107773	AC107773 Mus muscu	C 942	33.4	4.4	167248	10	AC141885	AC141885 Mus muscu
C 870	33.6	4.4	254594	2	AC132698	AC132698 Rattus no	C 943	33.4	4.4	167493	5	BX322607	BX322607 Zebrafish
C 871	33.6	4.4	261825	2	AC106351	AC106351 Rattus no	C 944	33.4	4.4	169500	2	AC138469	AC138469 Homo sapi
C 872	33.6	4.4	264410	10	AP0016119	AP0016119 Mus muscu	C 945	33.4	4.4	169693	9	HS57A13	Z83848 Human DNA s
C 873	33.6	4.4	286485	1	AP002557	AP002557 Escherich	C 946	33.4	4.4	169830	2	AC013345	AC013345 Homo sapi
C 874	33.6	4.4	295788	2	AC109126	AC109126 Rattus no	C 947	33.4	4.4	170916	9	AL136300	AL136300 Human DNA
875	33.6	4.4	308232	2	AL392004	AL392004 Homo sapi	C 948	33.4	4.4	171593	10	AL672074	AL672074 Mouse DNA
876	33.6	4.4	310122	2	AC126797	AC126797 Mus muscu	C 949	33.4	4.4	172314	2	AC026154	AC026154 Homo sapi
C 877	33.6	4.4	319367	10	AC021709	AC021709 Mus muscu	C 950	33.4	4.4	174383	2	AC012053	AC012053 Homo sapi
C 878	33.4	4.4	400	10	MMXWV9	Z46250 M.musculus	C 951	33.4	4.4	175179	10	AC134560	AC134560 Mus muscu
C 879	33.4	4.4	626	11	GE8719	GE8719 SHGC-105512	C 952	33.4	4.4	178660	9	HS61150	HS61150 Mus muscu
C 880	33.4	4.4	912	6	CQ646832	CQ646832 Sequence	C 953	33.4	4.4	179762	2	AC013519	AC013519 Homo sapi
C 881	33.4	4.4	918	10	AY318209	AY318209 Mus muscu	C 954	33.4	4.4	180885	2	AC110252	AC110252 Mus muscu
C 882	33.4	4.4	1572	8	AK1117417	AK1117417 Arabidops	C 955	33.4	4.4	180944	9	AC084855	AC084855 Homo sapi
C 883	33.4	4.4	2031	9	AB050429	AB050429 Macaca fa	C 956	33.4	4.4	182147	9	AC062032	AC062032 Homo sapi
C 884	33.4	4.4	5975	6	AX251790	AX251790 Sequence	C 957	33.4	4.4	183761	2	AC120450	AC120450 Rattus no
885	33.4	4.4	6558	6	CQ806878	CQ806878 Sequence	C 958	33.4	4.4	185581	10	AC132244	AC132244 Mus muscu
886	33.4	4.4	6558	6	CQ807152	CQ807152 Sequence	C 959	33.4	4.4	188735	10	AC111091	AC111091 Mus muscu
887	33.4	4.4	6558	6	AX251304	AX251304 Sequence	C 960	33.4	4.4	189236	10	AL607030	AL607030 Mouse DNA
888	33.4	4.4	6558	6	AX795814	AX795814 Sequence	C 961	33.4	4.4	192641	5	BX322588	BX322588 Zebrafish
889	33.4	4.4	6558	6	AX795930	AX795930 Sequence	C 962	33.4	4.4	193423	2	BX571851	BX571851 Danio rer
890	33.4	4.4	6558	6	AX822324	AX822324 Sequence	C 963	33.4	4.4	193963	9	AC013475	AC013475 Homo sapi
891	33.4	4.4	6558	6	AX822452	AX822452 Sequence	C 964	33.4	4.4	195880	2	AC149277	AC149277 Mus muscu
892	33.4	4.4	6558	6	AX825964	AX825964 Sequence	C 965	33.4	4.4	199917	2	AC006755	AC006755 Caenorhab
893	33.4	4.4	6558	6	AX826092	AX826092 Sequence	C 966	33.4	4.4	200461	9	AL592402	AL592402 Human DNA
C 894	33.4	4.4	9640	9	AC093375	AC093375 Homo sapi	C 967	33.4	4.4	204590	10	AC124738	AC124738 Mus muscu
C 895	33.4	4.4	10001	6	CQ807039	CQ807039 Sequence	C 968	33.4	4.4	208922	5	AL929017	AL929017 Zebrafish

969	33.4	4.4	208942	2	AC121011	AC121011 Rattus no	c1042	33.2	4.3	166354	2	AL929579	Danio rer
970	33.4	4.4	211986	5	BX511229	Zebrafish	c1043	33.2	4.3	166870	2	BX927276	Danio rer
971	33.4	4.4	212074	2	AC127787	Rattus no	1044	33.2	4.3	167181	2	AC131701	Mus muscu
972	33.4	4.4	213589	2	AC097281	Rattus no	c1045	33.2	4.3	186605	2	AC022477	Homo sapi
973	33.4	4.4	214779	2	AC112769	Rattus no	c1046	33.2	4.3	170022	9	AC024367	Homo sapi
974	33.4	4.4	221733	2	AC128906	Rattus no	1047	33.2	4.3	172350	2	AC079234	Homo sapi
975	33.4	4.4	221813	2	AC116707	Mus muscu	1048	33.2	4.3	174098	9	AC005737	Homo sapi
976	33.4	4.4	222940	2	AC097839	Rattus no	1049	33.2	4.3	175161	2	BX927396	Danio rer
977	33.4	4.4	223808	2	AC114139	Rattus no	1050	33.2	4.3	176470	9	AL353626	Human DNA
978	33.4	4.4	227022	2	AC149333	Strongylo	1051	33.2	4.3	176473	2	AC090986	Homo sapi
979	33.4	4.4	230155	2	AC114073	Rattus no	1052	33.2	4.3	176642	10	AC121987	Mus muscu
980	33.4	4.4	231200	2	AC113399	Homo sapi	c1053	33.2	4.3	176981	2	AC130261	Rattus no
981	33.4	4.4	232092	2	AC127800	Rattus no	1054	33.2	4.3	178387	10	AC121928	Mus muscu
982	33.4	4.4	232877	2	AC094618	Rattus no	1055	33.2	4.3	178704	9	BX119904	Human DNA
983	33.4	4.4	233796	2	AC130568	Rattus no	c1056	33.2	4.3	178824	9	AC146421	Human DNA
984	33.4	4.4	237732	2	AC127135	Rattus no	c1057	33.2	4.3	181413	9	AC080032	Homo sapi
985	33.4	4.4	238934	2	BX548160	Danio rer	c1058	33.2	4.3	182997	9	AL355332	Human DNA
986	33.4	4.4	240539	2	BX571803	Danio rer	c1059	33.2	4.3	183052	2	AC109892	Rattus no
987	33.4	4.4	241036	2	AC095383	Rattus no	1060	33.2	4.3	183946	2	AC009164	Homo sapi
988	33.4	4.4	248466	2	AC105146	Rattus no	1061	33.2	4.3	184144	9	AL451010	Human DNA
989	33.4	4.4	249995	3	AE014840	Plasmodiu	c1062	33.2	4.3	189589	2	AC146641	Otolemur
990	33.4	4.4	253918	2	AC106931	Rattus no	c1063	33.2	4.3	190806	2	AC115436	Rattus no
991	33.4	4.4	256635	2	AC128838	Rattus no	c1064	33.2	4.3	191046	10	AL607146	Mouse DNA
992	33.4	4.4	257518	2	AC118524	Rattus no	c1065	33.2	4.3	191684	2	AC018826	Homo sapi
993	33.4	4.4	260286	2	AC129651	Rattus no	c1066	33.2	4.3	191713	10	AC124397	Mus muscu
994	33.4	4.4	270264	2	AC103092	Rattus no	c1067	33.2	4.3	191964	2	AC119311	Rattus no
995	33.4	4.4	276343	2	AC125570	Rattus no	c1068	33.2	4.3	194160	2	AC131911	Mus muscu
996	33.4	4.4	300029	1	AE001297	Leptospir	1069	33.2	4.3	194372	9	AC019184	Homo sapi
997	33.4	4.4	340000	9	AF001691	Homo sapi	1070	33.2	4.3	194551	9	AC092291	Homo sapi
998	33.4	4.4	340000	9	AF001700	Homo sapi	1071	33.2	4.3	194892	2	CR376797	Danio rer
999	33.4	4.4	340000	9	AF001700	Homo sapi	c1072	33.2	4.3	195057	2	CR381708	Danio rer
1000	33.2	4.3	3519	11	G59093	SHGC-106668	c1073	33.2	4.3	196009	5	BX548045	Zebrafish
1001	33.2	4.3	664	11	G58955	SHGC-106725	1074	33.2	4.3	197139	2	AC141894	Mus muscu
1002	33.2	4.3	1055	6	AX083745	Sequence	c1075	33.2	4.3	198430	5	BX664716	Zebrafish
1003	33.2	4.3	13286	6	C8087296	Sequence	c1076	33.2	4.3	198949	9	AC010287	Homo sapi
1004	33.2	4.3	30849	3	AC117082	Dictyoste	1077	33.2	4.3	199287	2	AC068659	Homo sapi
1005	33.2	4.3	38240	3	CEB0491	Z49907 Caenorhabdi	c1078	33.2	4.3	201567	9	AC011901	Homo sapi
1006	33.2	4.3	38262	9	HGN98B6	Z68325 Human DNA s	c1079	33.2	4.3	202563	2	AC102479	Mus muscu
1007	33.2	4.3	47756	2	AC136356	Homo sapi	1080	33.2	4.3	205562	2	AC126511	Rattus no
1008	33.2	4.3	72751	9	AC090112	AC090112 Pan trogl	c1081	33.2	4.3	207906	2	BX927226	Danio rer
1009	33.2	4.3	93826	8	AC108876	AC108876 Oryza sat	1082	33.2	4.3	209243	2	BX119920	Danio rer
1010	33.2	4.3	95455	5	BX324232	Zebrafish	1083	33.2	4.3	220173	9	AC012183	Homo sapi
1011	33.2	4.3	114802	9	AC026230	AC026230 Homo sapi	c1084	33.2	4.3	220832	2	AC126145	Rattus no
1012	33.2	4.3	122049	5	BX649332	Zebrafish	c1085	33.2	4.3	222284	2	AC024442	Homo sapi
1013	33.2	4.3	127058	2	AC025652	AC025652 Homo sapi	1086	33.2	4.3	222728	2	AC141289	Homo sapi
1014	33.2	4.3	130088	9	AC110073	AC110073 Homo sapi	1087	33.2	4.3	223182	5	AL929049	Zebrafish
1015	33.2	4.3	132029	9	H8795623	AL031000 Human DNA	c1088	33.2	4.3	223306	10	AC125181	Mus muscu
1016	33.2	4.3	135224	2	AC022373	AC022373 Homo sapi	1089	33.2	4.3	225880	2	AC131693	Mus muscu
1017	33.2	4.3	136064	10	AL928992	AL928992 Mouse DNA	c1090	33.2	4.3	226735	2	AC121120	Mus muscu
1018	33.2	4.3	138710	10	AC033608	AC033608 Mus muscu	c1091	33.2	4.3	226837	2	AC142476	Rattus no
1019	33.2	4.3	143428	9	AL162587	AL162587 Human DNA	c1092	33.2	4.3	231303	2	BX649405	Danio rer
1020	33.2	4.3	143741	10	BX001009	BX001009 Mouse DNA	c1093	33.2	4.3	231868	2	AC118124	Rattus no
1021	33.2	4.3	144084	2	BX571682	BX571682 Danio rer	c1094	33.2	4.3	238379	2	AL590986	Homo sapi
1022	33.2	4.3	148851	9	HS155D22	Z97205 Human DNA s	c1095	33.2	4.3	244574	2	AC103190	Rattus no
1023	33.2	4.3	149818	2	AC105955	AC105955 Mus muscu	1096	33.2	4.3	245717	2	AC136281	Rattus no
1024	33.2	4.3	151802	3	AC114263	AC114263 Dictyoste	1097	33.2	4.3	249684	2	AC132983	Rattus no
1025	33.2	4.3	152158	2	BX649301	BX649301 Danio rer	1098	33.2	4.3	252614	5	BX255907	Zebrafish
1026	33.2	4.3	152181	9	AL391869	AL391869 Human DNA	1099	33.2	4.3	255917	2	AC112350	Rattus no
1027	33.2	4.3	152706	5	AL935302	AL935302 Zebrafish	c1100	33.2	4.3	258373	2	AC093995	Rattus no
1028	33.2	4.3	153495	2	AC115841	AC115841 Mus muscu	1101	33.2	4.3	263789	2	AC103242	Rattus no
1029	33.2	4.3	154085	2	BX537124	BX537124 Danio rer	c1102	33.2	4.3	266237	2	AC094800	Rattus no
1030	33.2	4.3	155540	5	BX324162	BX324162 Zebrafish	1103	33.2	4.3	277858	8	AC113643	Rattus no
1031	33.2	4.3	157583	5	BX571951	BX571951 Zebrafish	c1104	33.2	4.3	300794	8	AE016884	Remothec
1032	33.2	4.3	158327	2	BX927212	BX927212 Danio rer	1105	33.2	4.3	308918	2	AC128085	Rattus no
1033	33.2	4.3	158806	2	AL591132	AL591132 Homo sapi	1106	33.2	4.3	314016	2	AC146012	Pan trogl
1034	33.2	4.3	158963	2	AC141725	AC141725 Apis mell	1107	33.2	4.3	320398	2	AC136192	Rattus no
1035	33.2	4.3	160077	10	AC125354	AC125354 Mus muscu	1108	33.2	4.3	341050	3	PF929357	Plasmodiu
1036	33.2	4.3	160971	2	AC149568	AC149568 Papio anu	1109	33.2	4.3	343980	6	AX344556	Sequence
1037	33.2	4.3	164006	9	BX000449	BX000449 Human DNA	1110	33	4.3	304	6	CQ698694	Sequence
1038	33.2	4.3	164508	2	AC104130	AC104130 Homo sapi	1111	33	4.3	614	11	BV160444	RPAMMSQ0
1039	33.2	4.3	165062	9	AC087834	AC087834 Pan trogl	c1112	33	4.3	1010	8	AF159385	Hordemus b
1040	33.2	4.3	165695	2	CR352250	CR352250 Danio rer	1113	33	4.3	1078	3	AY368909	Synergus
1041	33.2	4.3	166253	9	AC008900	AC008900 Homo sapi	1114	33	4.3	1227	10	RNO250730	Rattus no

cl115	33	4.3	1391	6	AX878715	Sequence	1188	33	4.3	179055	3	AC093551	AC093551 Drosophil
cl116	33	4.3	1391	6	BD157402	Primer fo	cl189	33	4.3	179839	3	AC022342	AC022342 Drosophil
cl117	33	4.3	1391	6	AX021832	Homo sapi	cl190	33	4.3	184547	9	AC011626	AC011626 Homo sapi
cl118	33	4.3	1581	8	AF441395	Candida a	cl191	33	4.3	184716	2	AC026492	AC026492 Mus muscu
cl119	33	4.3	1602	6	AX506162	Sequence	cl192	33	4.3	185799	2	CR381553	CR381553 Danio rer
cl120	33	4.3	1683	8	AY081532	Arabidops	cl193	33	4.3	186279	10	AC121977	AC121977 Mus muscu
cl121	33	4.3	1763	8	AY054633	Arabidops	cl194	33	4.3	187533	5	BX950191	BX950191 Zebrafish
cl122	33	4.3	1908	8	ATH306961	Arabidops	cl195	33	4.3	193250	9	AC027238	AC027238 Homo sapi
cl123	33	4.3	2000	6	AX655393	Sequence	cl196	33	4.3	195621	2	AC133060	AC133060 Rattus no
cl124	33	4.3	3103	1	AF269420	Staphyloc	cl197	33	4.3	195771	2	AC091692	AC091692 Homo sapi
cl125	33	4.3	3103	6	AR485376	Sequence	cl198	33	4.3	196442	10	AL844584	AL844584 Mouse DNA
cl126	33	4.3	3103	6	AX144740	Sequence	cl199	33	4.3	196452	2	AC018869	AC018869 Homo sapi
cl127	33	4.3	3438	1	AF270201	Staphyloc	cl200	33	4.3	199131	2	AC027325	AC027325 Homo sapi
cl128	33	4.3	3438	6	AR486155	Sequence	cl201	33	4.3	199956	10	AC147241	AC147241 Mus muscu
cl129	33	4.3	3438	6	AX145519	Sequence	cl202	33	4.3	200823	9	AC009652	AC009652 Homo sapi
cl130	33	4.3	3463	6	AF269957	Staphyloc	cl203	33	4.3	202228	2	AC124646	AC124646 Mus muscu
cl131	33	4.3	3463	6	AR485911	Sequence	cl204	33	4.3	203521	2	AC146953	AC146953 Pongo pyg
cl132	33	4.3	3463	6	AX145275	Sequence	cl205	33	4.3	203058	5	AL844150	AL844150 Zebrafish
cl133	33	4.3	4578	9	BC038296	Homo sapi	cl206	33	4.3	204230	9	AC007318	AC007318 Homo sapi
cl134	33	4.3	7276	10	AL732549	Mouse DNA	cl207	33	4.3	205816	2	AC145411	AC145411 Bos tauru
cl135	33	4.3	9263	6	CQ592241	Sequence	cl208	33	4.3	206616	2	CNS00M8U	AL079351 Homo sapi
cl136	33	4.3	20576	2	AC014212	Drosophil	cl209	33	4.3	206837	10	AC124733	AC124733 Mus muscu
cl137	33	4.3	21460	9	AL589927	Human DNA	cl210	33	4.3	208961	2	AC125450	AC125450 Mus muscu
cl138	33	4.3	27108	1	AL550767	Sequence	cl211	33	4.3	211680	2	CR385082	CR385082 Danio rer
cl139	33	4.3	37208	5	AF090120	Fugu rubr	cl212	33	4.3	214520	2	AC125256	AC125256 Mus muscu
cl140	33	4.3	60612	2	AC135632	Homo sapi	cl213	33	4.3	214678	2	CR388060	CR388060 Danio rer
cl141	33	4.3	61653	8	AP006681	Lotus cor	cl214	33	4.3	217073	2	AC114144	AC114144 Rattus no
cl142	33	4.3	67033	9	AL137008	Human DNA	cl215	33	4.3	218023	2	AC115925	AC115925 Mus muscu
cl143	33	4.3	70331	2	AC120037	Homo sapi	cl216	33	4.3	220874	2	CR376848	CR376848 Danio rer
cl144	33	4.3	73549	2	AC020104	Drosophil	cl217	33	4.3	222938	2	AC095075	AC095075 Rattus no
cl145	33	4.3	85980	5	AL591671	Zebrafish	cl218	33	4.3	224144	2	AC107714	AC107714 Mus muscu
cl146	33	4.3	90963	5	AC012602	Homo sapi	cl219	33	4.3	224802	2	AC006787	AC006787 Caenorhab
cl147	33	4.3	101173	8	CNS008C8V	Oryza sat	cl220	33	4.3	226225	2	AC121002	AC121002 Rattus no
cl148	33	4.3	103192	8	AC007369	Arabidops	cl221	33	4.3	227993	10	AL645930	AL645930 Mouse DNA
cl149	33	4.3	105468	8	AP004852	Oryza sat	cl222	33	4.3	236685	2	AC131318	AC131318 Mus muscu
cl150	33	4.3	110000	8	CR381622	Mus muscu	cl223	33	4.3	237992	2	AC102617	AC102617 Mus muscu
cl151	33	4.3	110000	8	CR381622	Continuation (7 of	cl224	33	4.3	240729	2	AC111961	AC111961 Rattus no
cl152	33	4.3	119119	9	AC008970	Homo sapi	cl225	33	4.3	241498	10	AC098137	AC098137 Mus muscu
cl153	33	4.3	120548	3	AC024798	Caenorhab	cl226	33	4.3	244435	2	AC084021	AC084021 Mus muscu
cl154	33	4.3	125566	2	AC069447	Mus muscu	cl227	33	4.3	245156	2	AC095956	AC095956 Rattus no
cl155	33	4.3	125729	6	AX818232	Sequence	cl228	33	4.3	248087	2	AC095277	AC095277 Rattus no
cl156	33	4.3	125729	9	HS971N18	Human DNA	cl229	33	4.3	249281	2	AC095956	AC095956 Rattus no
cl157	33	4.3	127266	9	AC023672	Homo sapi	cl230	33	4.3	249636	10	AC099741	AC099741 Mus muscu
cl158	33	4.3	128447	2	AC006490	Drosophil	cl231	33	4.3	252146	2	AC118155	AC118155 Rattus no
cl159	33	4.3	136988	9	AC093699	Homo sapi	cl232	33	4.3	254542	2	AC124321	AC124321 Mus muscu
cl160	33	4.3	139278	5	EX001001	Zebrafish	cl233	33	4.3	259871	2	AC107164	AC107164 Rattus no
cl161	33	4.3	139394	2	AC010046	Drosophil	cl234	33	4.3	260987	2	AC121031	AC121031 Rattus no
cl162	33	4.3	140186	2	AC055808	Homo sapi	cl235	33	4.3	280115	2	AC105710	AC105710 Rattus no
cl163	33	4.3	142694	2	AC078966	Homo sapi	cl236	33	4.3	282895	2	AL133478	AL133478 Homo sapi
cl164	33	4.3	145635	8	AP004787	Oryza sat	cl237	33	4.3	293161	2	BX908750	BX908750 Danio rer
cl165	33	4.3	148168	2	AC146785	Medicago	cl238	33	4.3	295920	2	AC108611	AC108611 Rattus no
cl166	33	4.3	149724	4	AC129888	Atelerix	cl239	33	4.3	300787	1	AE016744	AE016744 Staphyloc
cl167	33	4.3	149806	10	AC105159	Mus muscu	cl240	33	4.3	314896	2	AC091357	AC091357 Rattus no
cl168	33	4.3	158921	9	AC024329	Homo sapi	cl241	33	4.3	315098	3	AE003495	AE003495 Drosophil
cl169	33	4.3	159476	9	AL441963	Human DNA	cl242	33	4.3	322554	3	AE003592	AE003592 Drosophil
cl170	33	4.3	159715	9	AC011978	Homo sapi	cl243	33	4.3	336376	2	AC106127	AC106127 Rattus no
cl171	33	4.3	161508	2	BX927222	Danio rer	cl244	32.8	4.3	387	10	BNUS5800	US9800 Rattus norv
cl172	33	4.3	161612	9	AC020754	Homo sapi	cl245	32.8	4.3	408	6	AX300942	AX300942 Sequence
cl173	33	4.3	162172	8	AC140026	Medicago	cl246	32.8	4.3	685	11	G56885	G56885 SHGC-102618
cl174	33	4.3	162566	9	AC103724	Homo sapi	cl247	32.8	4.3	807	11	BV154605	BV154605 ESRI_43 R
cl175	33	4.3	164394	2	AC022873	Homo sapi	cl248	32.8	4.3	7546	1	AY082011	AY082011 Enterococ
cl176	33	4.3	164434	2	AC009841	Homo sapi	cl249	32.8	4.3	9010	14	AF178440	AF178440 Triatoma
cl177	33	4.3	164853	2	AC022343	Drosophil	cl250	32.8	4.3	11173	9	AC126173	AC126173 Homo sapi
cl178	33	4.3	164906	2	AC119059	Bos tauru	cl251	32.8	4.3	11181	9	AC128679	AC128679 Homo sapi
cl179	33	4.3	168776	5	EX465204	Zebrafish	cl252	32.8	4.3	15361	4	OCRRR	X15750 Rabbit skel
cl180	33	4.3	170040	10	AC125360	Mus muscu	cl253	32.8	4.3	15823	4	OCRRR	X15209 O.cunicul
cl181	33	4.3	170919	2	AL120358	Homo sapi	cl254	32.8	4.3	38194	5	BX571725	BX571725 Carp DNA
cl182	33	4.3	172883	9	AL391374	Human DNA	cl255	32.8	4.3	38589	9	AC068994	AC068994 Homo sapi
cl183	33	4.3	173993	9	AC009230	Homo sapi	cl256	32.8	4.3	39210	3	U41508	U41508 Caenorhabd
cl184	33	4.3	177806	9	AC093106	Homo sapi	cl257	32.8	4.3	45434	10	AL805979	AL805979 Mouse DNA
cl185	33	4.3	177921	2	AC112343	Rattus no	cl258	32.8	4.3	47268	2	AC020414	AC020414 Drosophil
cl186	33	4.3	178553	2	AC006891	Caenorhab	cl259	32.8	4.3	58972	2	AC137725	AC137725 Mus muscu
cl187	33	4.3	178965	3	AC010117	Drosophil	cl260	32.8	4.3	63601	9	AC080135	AC080135 Homo sapi

1261 32.8 4.3 72143 2 AC016006 AC016006 Homo sapi
 c1262 32.8 4.3 72751 9 AC090112 AC090112 Pan trogl
 1263 32.8 4.3 73162 9 AC105095 AC105095 Homo sapi
 1264 32.8 4.3 87084 5 BX001047 BX001047 Zebrafish
 c1265 32.8 4.3 90479 8 AC121463_3 AC121463_3
 1266 32.8 4.3 91570 8 AT113K14 AT113K14
 1267 32.8 4.3 98630 8 AC006535 AC006535
 1268 32.8 4.3 104309 8 AC138717 AC138717 Human DNA
 1269 32.8 4.3 110000 1 AE017355_22 AE017355_22
 c1270 32.8 4.3 110000 10 AE017355_22 AE017355_22
 1271 32.8 4.3 110000 10 AE017355_22 AE017355_22
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RESULT 2
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LOCUS
DEFINITION
Sequence 47 from Patent WO0116318.
ACCESSION
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VERSION
AX092316.1 GI:13444472
KEYWORDS
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SOURCE
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ORGANISM
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Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1
Eaton, D.L., Filvaroff, E., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Grimaldi, C.J., Gurney, A.L., Watanabe, C.K. and
Wood, W.I.
Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL
Patent: WO 0116318-A 47 08-MAR-2001;
Genentech, Inc. (US)
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Best Local Similarity 100.0%; Pred. No. 2.7e-208;
Matches 766; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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LOCUS
DEFINITION
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ACCESSION
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VERSION
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ORGANISM
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Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1
Baker, K.P., Chen, J., Desnoyers, L., Goddard, A., Godowski, P.J.,
Gurney, A.L., Pan, J., Smith, V., Watanabe, C.K., Wood, W.I. and
Zhang, Z.
Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL
Patent: WO 0168848-A 197 20-SEP-2001;
Genentech, Inc. (US)
FEATURES
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Best Local Similarity 100.0%; Pred. No. 2.7e-208;
Matches 766; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE			
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AUTHORS			
Ashkenazi, A. J., Baker, K. P., Botstein, D., Deanov, L., Eaton, D.,			
Ferrara, N., Gerber, H., Gerritsen, M., Goddard, A., Godowski, P.,			
Grimaldi, C. J., Gurney, A. L., Kijavits, I., Napier, M. A., Pan, J.,			
Paoni, N. F., Roy, M., Stewart, T. A., Tamas, D., Watanabe, C. K.,			
Williams, P., Wood, W. I., and Zhang, Z.			
TITLE			
Secreted and transmembrane polypeptides and nucleic acids encoding			
the same			
JOURNAL			
Patent: WO 0073454-A 257 07-DEC-2000;			
Genentech Inc. (US)			
FEATURES			
Location/Qualifiers			

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				VERSION		AY358671.1		GI:37182463	
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 766)
Clark.H.F., Gurney.A.L., Abaya.E., Baker.K., Baldwin.D., Brush.J.,
Chen.J., Chow.B., Chui.C., Crowley.C., Currell.B., Deuel.B.,
Dowd.P., Eaton.D., Foster.J., Grimaldi.C., Gu.Q., Hass.P.E.,
Heldens.S., Huang.A., Kim.H.S., Klinowski.L., Jin.Y., Johnson.S.,
Lee.J., Lewis.L., Liao.D., Mark.M., Robbie.E., Sanchez.C.,
Schoenfeld.J., Seshagiri.S., Simmons.L., Singh.J., Smith.V.,
Stinson.J., Vagts.A., Vandlen.R., Watanabe.C., Wieand.D., Woods.K.,
Xie.M.H., Yasura.D., Yi.S., Yu.G., Yuan.J., Zhang.M., Zhang.Z.,
Goddard.A., Wood.W.I. and Godowski.P.
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
Effort to Identify Novel Human Secreted and Transmembrane Proteins:
A Bioinformatics Assessment
Genome Res. 13 (10), 2265-2270 (2003)
12975309

2 (bases 1 to 766)
Clark.H.F.
Direct Submission
Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
Inc., 1 DNA Way, South San Francisco, CA 94080, USA

JOURNAL
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
Inc., 1 DNA Way, South San Francisco, CA 94080, USA

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ACCESSION AK026453
VERSION AK026453.1 GI:10439322
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Kawakami,T., Noguchi,S., Itoh,T., Shigeta,K., Senba,T.,
Matsumura,K., Nakajima,Y., Mizuno,T., Morinaga,M., Tanigami,A.,
Fujiwara,T., Ono,T., Yamada,K., Fujii,Y., Ozaki,K., Hirao,M.,
Ohmori,Y., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T.,
Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
NEDO human cDNA sequencing project
Unpublished
2 (bases 1 to 2308)
Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T.,
Shibahara,T., Tanaka,T. and Nakamura,Y.
Direct Submission
Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Laboratory of Genome Structure Analysis, Human
Genome Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639,
Japan (E-mail:flcdna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
Fax:81-3-5449-5416)
COMMENT NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing; Research Association for Biotechnology; cDNA library
construction, 5'- & 3'-end one pass sequencing; Department of
Virology and Human Genome Center, Institute of Medical Science,
University of Tokyo (partly supported by Science and Technology
Agency).
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DEFINITION	Homo sapiens clone RP11-395L7, LOW-PASS SEQUENCE SAMPLING.								
ACCESSION	AC079784								
VERSION	AC079784.1 GI:10048030								

KEYWORDS	HTG; HTGS_PHASE0.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE	1 (bases 1 to 46778)
JOURNAL	Waterston,R.H.
REFERENCE	The sequence of Homo sapiens clone
AUTHORS	Unpublished
TITLE	2 (bases 1 to 46778)
JOURNAL	Waterston,R.H.
COMMENT	Direct Submission Submitted (10-SEP-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA Center project name: H.NH0395L07. * NOTE: This record contains 85 individual * sequencing reads that have not been assembled into * contigs. Runs of N are used to separate the reads * and the order in which they appear is completely * arbitrary. Low-pass sequence sampling is useful for * identifying clones that may be gene-rich and allows * overlap relationships among clones to be deduced. * However, it should not be assumed that this clone * will be sequenced to completion. In the event that * the record is updated, the accession number will * be preserved. * 1 881: contig of 881 bp in length * 882 891: gap of unknown length * 892 1193: contig of 302 bp in length * 1194 1203: gap of unknown length * 1204 1745: contig of 542 bp in length * 1746 1755: gap of unknown length * 1756 2630: contig of 875 bp in length * 2631 2640: gap of unknown length * 2641 3507: contig of 867 bp in length * 3508 3517: gap of unknown length * 3518 4441: contig of 924 bp in length * 4442 4521: gap of unknown length * 4522 4972: contig of 521 bp in length * 4973 4982: gap of unknown length * 4983 5891: contig of 909 bp in length * 5892 5901: gap of unknown length * 5902 6445: contig of 544 bp in length * 6446 6455: gap of unknown length * 6456 6943: contig of 488 bp in length * 6944 6953: gap of unknown length * 6954 7494: contig of 541 bp in length * 7495 7504: gap of unknown length * 7505 7970: contig of 466 bp in length * 7971 7980: gap of unknown length * 7981 8845: contig of 865 bp in length * 8846 8855: gap of unknown length * 8856 9297: contig of 442 bp in length * 9298 9307: gap of unknown length * 9308 10207: contig of 900 bp in length * 10208 10217: gap of unknown length * 10218 10625: contig of 408 bp in length * 10626 10635: gap of unknown length * 10636 11468: contig of 833 bp in length * 11469 11478: gap of unknown length * 11479 11996: contig of 518 bp in length * 11997 12006: gap of unknown length * 12007 12502: contig of 496 bp in length * 12503 12512: gap of unknown length * 12513 12968: contig of 456 bp in length * 12969 12978: gap of unknown length * 12979 13496: contig of 518 bp in length * 13497 13506: gap of unknown length * 13507 14048: contig of 542 bp in length * 14049 14058: gap of unknown length * 14059 14426: contig of 368 bp in length * 14427 14436: gap of unknown length

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Best Local Similarity

Matches 341; Conservative

43.1%; Score 332; DB 2; Length 46778;

95.8%; Pred. No. 6.9e-84;

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RESULT 9
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DEFINITION AX246020
ACCESSION AX246020
VERSION AX246020.1 GI:15860694
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Williams,L.T., Escobedo,J., Innis,M.A., Garcia,P.D.,
Sudduth-Klinger,J., Reinhard,C., Randazzo,F., Kennedy,G.C., Pot,D.,
Kassam,A., Lamson,G., Drmanac,R., Crkvenjakov,R., Dickson,M.,
Drmanac,S., Labat,I., Leshkowitz,D., Kita,D., Garcia,V. and
Stache-Grain,B.
TITLE Human genes and gene expression products
JOURNAL Patent: WO 0166753-A 950 13-SEP-2001;
Chiron Corporation (US); Hyseq Inc. (US)
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ORIGIN
Query Match 34.5%; Score 264.2; DB 6; Length 351;
Best Local Similarity 91.0%; Pred. No. 1.9e-64;
Matches 303; Conservative 0; Mismatches 28; Indels 2; Gaps 2;

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QY 67 TTCAGCCTGCTGGTTCTACTGCTGTAGGAGTAGTTCTCAATGCGATACCT-CTAATTGT 125
DB 78 CTCAACTGCTGCTTTTACTGCTGTGGTAGGAGTGTCTCACTCGACACCTGCTAATTGT 137
QY 126 CAGCTTAGTT-GAGGAAGACCAATTTTCTCAAAACCCCATCTCTTGTGAGTGGTGGT 184
DB 138 CATATTATTTAGAGGAAGACCAATTTGTCCTCAAAAGCCCATCTCTTGTGAGTGGTGGT 197
QY 185 TCCAGGAATTATAGGAGCAGGTCTGATGGCCATTCCAGCAACCAATGTCCTTGACAG 244
DB 198 TCCACGAATTATAGAGGAGGCTGTGATGCCATTCCAGCAACCAATGTCCTTGACAG 257
QY 245 CAAGAAAAAGAGCGTGTGCAACACAGAACTGGAATGTTTCTTTCATCATTTTTCAGTG 304
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Db 318 TGATCACAGTCATGTTGGTGTCTGTATTGTCATGC 350
RESULT 10
AX098190
LOCUS AX098190 286 bp DNA linear PAT 30-MAR-2001
DEFINITION Sequence 102 from Patent WO0118542.
ACCESSION AX098190
VERSION AX098190.1 GI:13515269
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE Lee, J., Thompson, P. and Lillie, J.
JOURNAL Identification, assessment, prevention, and therapy of ovarian
FEATURES cancer
Patent: WO 0118542-A 102 15-MAR-2001;
Millennium Predictive Medicine, Inc. (US)
FEATURES Location/Qualifiers
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Best Local Similarity 99.6%; Pred. No. 4.7e-55;
Matches 212; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 7 AGCGTTTCTGAGCCAGGGTGACCATGACCTGCTGCGAAGGATGGACATCTCGCAATGGA 66
DB 48 AACGTTTCTGAGCCAGGGTGACCATGACCTGCTGCGAAGGATGGACATCTCGCAATGGA 107
QY 67 TTCAGCCTCTGCTTCTACTGCTGTGTAGGAGTAGTTCTCAATGCGATACCTCTAATGTC 126
DB 108 TTCAGCCTCTGCTTCTACTGCTGTGTAGGAGTAGTTCTCAATGCGATACCTCTAATGTC 167
QY 127 ACCTTAGTTGAGGAGAGACCAATTTCTCAAAACCCATCTCTGTTGAGTGGTGGTTC 186
DB 168 ACCTTAGTTGAGGAGAGACCAATTTCTCAAAACCCATCTCTGTTGAGTGGTGGTTC 227
QY 187 CCAGGAATATAGGAGCAGGTCTGATGGCCATTCAGCAACCAACATGTCCTT 239
DB 228 CCAGGAATATAGGAGCAGGTCTGATGGCCATTCAGCAACCAACATGTCCTT 280
RESULT 11
CQ741848
LOCUS CQ741848 201 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 27782 from Patent WO02068579.
ACCESSION CQ741848
VERSION CQ741848.1 GI:42350908
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
Patent: WO 02068579-A 27782 06-SEP-2002;
PE Corporation (NY) (US)
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DB 61 TTAGGAGTAGTTCTCAATGCGATACCTCTAAATTGTCAGCTTAGTTGAGGAAGACCAATTT 120
QY 151 TCTCAAAACCCCATCTCTTGTGTTGAGTGGTGGTTCCTCCAGGAATATAGAGAGAGTCTG 210
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QY 211 ATGG 214
DB 181 ATGG 184
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DEFINITION Mus musculus chromosome 1, clone RP23-404A6, complete sequence.
ACCESSION AC138214
VERSION AC138214.8 GI:50284610
KEYWORDS HTG.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE Birren, B., Nusbaum, C. and Lander, E.
JOURNAL 1 (bases 1 to 203478)
REFERENCE Mus musculus chromosome 1, clone RP23-404A6
2 (bases 1 to 203478)
Unpublished
Birken, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,
Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L., Boukhgalter, B.,
Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A.,
Cook, A., Cooke, P., DeArelano, K., Dewar, K., Diaz, J.S., Dodge, S.,
Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J.,
Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hafez, N.,
Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R.,
Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J.,
Mathews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T.,
Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C.,
Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J.,
Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R.,
Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schuback, R.,
Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N.,
Stojanovic, N., Talamas, J., Testfay, S., Theodore, J., Topham, K.,
Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X.,
Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (20-DEC-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 203478)
Birken, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,
Anderson, S., Bastien, V., Bloom, T., Boguslavskiy, L., Boukhgalter, B., Camarata, J., Chang, J.,
Choepel, Y., Collymore, A., Cooke, P., Corum, B.,
DeArelano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L.,
Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D.,
Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N.,
Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I.,
Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T.,
Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R.,
MacLean, C., Macdonald, P., Major, J., Manning, J., Mathews, C.,
McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V.,
Murphy, T., Naylor, J., Nguyen, C., Nguyen, T., Nicol, R., Norbu, C.,
O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K.,
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Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V. S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission
Submitted (19-MAY-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
4 (bases 1 to 203478)

Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Anderson, S., Arachchi, H. M., Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J. S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Nguyen, T., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V. S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission
Submitted (14-JUL-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 14, 2004 this sequence version replaced gi:47498220.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center -----
Center: Whitehead Institute/MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@broad.mit.edu
----- Project Information -----
Center project name: L28766
Center clone name: 404_A_6

TITLE
JOURNAL

COMMENT

FEATURES
source

Location/Qualifiers
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QY 609 AGGTCTATTGCTTGTGGAAATCTCGAGGTCTCTTGGGCTCAGTCAGTATAGTCATCGG 668
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RESULT 13
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LOCUS
DEFINITION Rattus norvegicus clone CH230-133G12, *** SEQUENCING IN PROGRESS
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 209326)
Muzny,D,Marie., Metzker,M,Lee., Abramzon,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
Biswal,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
Gebregorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
Hernandez,R., Hines,S., Hladun,S.L., Hodgson,N., Hognes,M.,
Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A.,
Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jollivet,A.,
Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,D., Kovar,C.,
Kowis,C., Kratt,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
Lorensuhewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J.,
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Mareshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A.,
Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
Mawhney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,
Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S.,
Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Naif,L.,
Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
Nwackelmeleh,O., Okwuonu,G., Olarpunagoon,A., Pal,S., Parks,K.,
Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkuch,C.,
Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L.,
Puzo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,
Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,
Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,
Sander,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,
Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D.,
Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,
Steinle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C.,
Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Umani,K.,
Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J.,
Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
Williams,G., Willison,R., Wleczyk,R., Wooden,H., Worley,K.,
Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
Yu,P., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Weinstock,G. and Gibbs,R.A.
Direct Submission
Unpublished
2 (bases 1 to 209326)
Worley,K.C.
Direct Submission
Submitted (12-JAN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 209326)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (13-MAY-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On May 13, 2003 this sequence version replaced gi:24942449.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GKVI
Center clone name: CH230-133G12
----- Summary Statistics
Assembly program: Atlas 3.0;
Consensus quality: 204322 bases at least Q40
Consensus quality: 205593 bases at least Q30
Consensus quality: 206229 bases at least Q20
Estimated insert size: 213275; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
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* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
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* runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

* 1 205655: contig of 205655 bp in length
 * 205656 205755: gap of unknown length
 * 205756 209326: contig of 3571 bp in length.

FEATURES

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ORIGIN

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 Best Local Similarity 78.7%; Pred. No. 6.3e-37;
 Matches 229; Conservative 0; Mismatches 53; Indels 9; Gaps 2;
 Qy 429 CAGTGCATTCATCCAGATCTCTCACTTGCAGTGGTTTTCATGACTCTTGTGCACC 488
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 Qy 489 TCCTACTGTTTCAATPAACCCACCATGTAACACACCATGCGAGTGGCTGGAGAGCATC 548
 Db 21804 TCCTACTGATTTTAAACACCCAC---TATCAACACATGTCAGTAACTTGAATAACC 21860
 Qy 549 TAGTTTCCACTCGATCTTGAGAAACCAACATAGGCTTATCCACTTCTCAGTATTTTT 608
 Db 21861 -----CAACTCAACTCTGAAGAAGACAGACAGAGATTTTCCACTTCTCAGTGTATT 21914
 Qy 609 AGTCTATTGCTTGTGGAAATCTGAGGCTCTGTTGGGCTCAGTCAGATGATGATCGG 668
 Db 21915 GAGTCTCTCTGTTGTGGATCTCTGAGCTCTGTTGGGCTTAGTCAGATCATTTGG 21974
 Qy 669 TTTCCTTGCTGCTGTGTGGAGTCTCTAAGCGAAGAGTCAAAATGTGTA 719
 Db 21975 TTTCCTTGCTGCTGTGTGGGCTCTCTCAGCGACGAGACAAATTTGATA 22025

RESULT 14

AC103323/c
 LOCUS Rattus norvegicus clone CH230-113N18, WORKING DRAFT SEQUENCE, 7
 DEFINITION 257693 bp DNA linear HTG 10-OCT-2002
 AC103323
 VERSION AC103323.4 GI:23664726
 KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 257693)

REFERENCE

AUTHORS Muzny, D. Marie., Metzker, M. Lee., Abramson, S., Adams, C., Alder, J.,
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 Direct Submission
 Unpublished
 2 (bases 1 to 257693)
 Worley, K. C.
 Direct Submission
 Submitted (24-NOV-2001) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 257693)
 Rat Genome Sequencing Consortium.
 Direct Submission
 Submitted (10-OCT-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Oct 10, 2002 this sequence version replaced gi:21731772.
 The sequence in this assembly is a combination of BAC based reads
 and whole genome shotgun sequencing reads assembled using Atlas
 (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described
 in the feature table below represents a scaffold in the Atlas
 assembly (a 'contig-scaffold'). Within each contig-scaffold,
 individual sequence contigs are ordered and oriented, and separated
 by sized gaps filled with Ns to the estimated size. The sequence
 may extend beyond the ends of the clone and there may be sequence
 contigs within a contig-scaffold that consist entirely of whole
 genome shotgun sequence reads. Both end sequences and whole genome
 shotgun sequence only contigs will be indicated in the feature
 table.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GKWI

Center clone name: CH230-113N18

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Run on: January 24, 2005, 19:10:32 ; Search time 334 Seconds
        (without alignments)
        12039.091 Million cell updates/sec

Title: US-10-063-553-47
Perfect score: 766
Sequence: 1 ggtcagaggttcttgagc.....agtagttgaaaaaaaaa 766
Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0
                Total number of hits satisfying chosen parameters: 8269772
                Minimum DB seq length: 0
                Maximum DB seq length: 200000000
                Post-processing: Minimum Match 0%
                               Maximum Match 100%
                               Listing first 1500 summaries
Database : N Geneseq_23Sep04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
SUMMARIES
No. Score Match Length DB ID Description
RESULT 1
ID AAZ65043 standard; cDNA; 766 BP.
DE Membrane-bound protein PRO994 encoding cDNA.
PN WO9963088-A2.
PD 09-DEC-1999.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 3; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 2
ID AAS46023 standard; cDNA; 766 BP.
DE Human DNA encoding PRO polypeptide sequence #99.
PN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 4; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 3
ID AAF92081 standard; cDNA; 766 BP.
DE Human PRO994 cDNA.
PN WO200116318-A2.
PD 08-MAR-2001.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 4; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 4
ID AAF44189 standard; cDNA; 766 BP.
DE Human PRO994 (UNQ518) nucleotide sequence SEQ ID NO:257.
PN WO200073454-A1.
PD 07-DEC-2000.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 5; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 5
ID ABS74401 standard; cDNA; 766 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO994.
PN US2002119130-A1.
PD 29-AUG-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 6; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 6
ID ACA89473 standard; cDNA; 766 BP.
DE cDNA encoding human PRO polypeptide #99.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 7
ID ACA73483 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 8
ID ACA05798 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 9
ID ACA66632 standard; cDNA; 766 BP.
DE cDNA encoding human PRO protein #99.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 10
ID ACA64335 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US200303531-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 11
ID ACA91187 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 12
ID ACD81564 standard; cDNA; 766 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO994.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 13
ID ACF20207 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 14
ID ACF19593 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 15
ID ACD21881 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
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PN US2003027267-A1.
 PD 06-FEB-2003.
 Query Match
 Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
 RESULT 16
 ID ACF13046 standard; cDNA; 766 BP.
 DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
 PN US2003036160-A1.
 PD 20-FEB-2003.
 Query Match
 Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
 RESULT 17
 ID ACD25149 standard; cDNA; 766 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #99.
 PN US2003044925-A1.
 PD 06-MAR-2003.
 Query Match
 Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
 RESULT 18
 ID ACF00198 standard; cDNA; 766 BP.
 DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
 PN US2003054474-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
 RESULT 19
 ID ACA60386 standard; cDNA; 766 BP.
 DE Novel human secreted and transmembrane protein PRO994 cDNA.
 PN US2003018183-A1.
 PD 23-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
 RESULT 20
 ID ACA72255 standard; cDNA; 766 BP.
 DE Novel human secreted and transmembrane protein PRO994 cDNA.
 PN US2003032114-A1.
 PD 13-FEB-2003.
 Query Match
 Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
 RESULT 21
 ID ACD04779 standard; cDNA; 766 BP.
 DE Novel human secreted and transmembrane protein PRO994 cDNA.
 PN US2003032101-A1.
 PD 13-FEB-2003.
 Query Match
 Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
 RESULT 22
 ID ACD18240 standard; cDNA; 766 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #99.
 PN US2003036124-A1.
 PD 20-FEB-2003.
 Query Match
 Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
 RESULT 23
 ID ACD08247 standard; cDNA; 766 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #99.
 PN US2003040054-A1.
 PD 27-FEB-2003.
 Query Match
 Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
 RESULT 24
 ID ACA88681 standard; cDNA; 766 BP.
 DE Novel human secreted and transmembrane protein PRO994 cDNA.
 PN US2003036133-A1.
 PD 20-FEB-2003.
 Query Match
 Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
 RESULT 25
 ID ACA70123 standard; cDNA; 766 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #99.
 PN US2003036134-A1.

PD 20-FEB-2003.
 Query Match
 Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
 RESULT 26
 ID ACD12345 standard; cDNA; 766 BP.
 DE Novel human secreted and transmembrane protein PRO994 cDNA.
 PN US2003022294-A1.
 PD 30-JAN-2003.
 Query Match
 Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
 RESULT 27
 ID ACC74260 standard; cDNA; 766 BP.
 DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
 PN US2003027275-A1.
 PD 06-FEB-2003.
 Query Match
 Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
 RESULT 28
 ID ACD15888 standard; cDNA; 766 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #99.
 PN US2003027324-A1.
 PD 06-FEB-2003.
 Query Match
 Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
 RESULT 29
 ID ACD25456 standard; cDNA; 766 BP.
 DE Novel human secreted and transmembrane protein PRO994 cDNA.
 PN US2003036118-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
 RESULT 30
 ID ACD17933 standard; cDNA; 766 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #99.
 PN US2003036123-A1.
 PD 20-FEB-2003.
 Query Match
 Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
 RESULT 31
 ID AC88220 standard; cDNA; 766 BP.
 DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
 PN US2003036148-A1.
 PD 20-FEB-2003.
 Query Match
 Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
 RESULT 32
 ID ACD21574 standard; cDNA; 766 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #99.
 PN US2003040060-A1.
 PD 27-FEB-2003.
 Query Match
 Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
 RESULT 33
 ID ACD18641 standard; cDNA; 766 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #99.
 PN US2003044916-A1.
 PD 06-MAR-2003.
 Query Match
 Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
 RESULT 34
 ID ACA58833 standard; cDNA; 766 BP.
 DE cDNA encoding human secreted polypeptide PRO994.
 PN US2003013855-A1.
 PD 16-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
 RESULT 35
 ID ABX98251 standard; cDNA; 766 BP.
 DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 197.
 PN US2003036156-A1.
 PD 20-FEB-2003.

Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 36
ID ACC91092 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 37
ID ACC9782 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 38
ID ACC88527 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 39
ID ACD21267 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 40
ID ABX75639 standard; cDNA; 766 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO994.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 41
ID ACA64009 standard; cDNA; 766 BP.
DE cDNA encoding human PRO polypeptide #24.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 42
ID ABX97842 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #99.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 43
ID ACA97318 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 44
ID ACA57781 standard; cDNA; 766 BP.
DE Human PRO994 cDNA.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 45
ID ACD14309 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #99.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;

Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 46
ID ACC91092 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 47
ID ACC8834 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 48
ID ACD07031 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #99.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 49
ID ACA67482 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #99.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 50
ID ACC81537 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 51
ID ACA91273 standard; cDNA; 766 BP.
DE cDNA encoding human PRO polypeptide #24.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 52
ID ACC89141 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 53
ID ACC86497 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 54
ID ACC89755 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 55
ID ACC92934 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
RESULT 56
ID ABX80794 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein CDNA, #103.
PN US2003027182-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
RESULT 57
ID ACA72562 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #99.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
RESULT 58
ID ACA89080 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
RESULT 59
ID ACA69816 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
RESULT 60
ID ACA96959 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
RESULT 61
ID ACA90955 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
RESULT 62
ID ACA70737 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
RESULT 63
ID ACA95247 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
RESULT 64
ID ACDA4303 standard; cDNA; 766 BP.
DE cDNA encoding human PRO994 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
RESULT 65
ID ACC86190 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;

Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 66
ID ACDA5172 standard; cDNA; 766 BP.
DE Human secreted/transmembrane polypeptide PRO994 cDNA.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
RESULT 67
ID ACC90062 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
RESULT 68
ID ACD12670 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
RESULT 69
ID ACF19900 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
RESULT 70
ID ABX76844 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #99.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
RESULT 71
ID ACA73176 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
RESULT 72
ID ACA68719 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
RESULT 73
ID ACA74563 standard; cDNA; 766 BP.
DE cDNA encoding human PRO polypeptide #99.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
RESULT 74
ID ACA70430 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
RESULT 75
ID ACD14616 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #99.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
RESULT 76
ID ACDA4303 standard; cDNA; 766 BP.
DE cDNA encoding human PRO994 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;

ID ACA93720 standard; cDNA; 766 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO994.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 77
ID ACA68288 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 78
ID ABX98753 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 79
ID ACA67294 standard; cDNA; 766 BP.
DE cDNA encoding human secreted polypeptide PRO994.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 80
ID ACC81230 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 81
ID ACA95554 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 82
ID ACD04472 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 83
ID ACC87913 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 84
ID ACF12575 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 85
ID ACH66267 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;

RESULT 86
ID ABX79474 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein cDNA, #103.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 87
ID ACA96290 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #99.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 88
ID ACA65064 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #99.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 89
ID ACA73790 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 90
ID ACA74202 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 91
ID ACA96597 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #99.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 92
ID ACD10703 standard; cDNA; 766 BP.
DE cDNA encoding human PRO polypeptide #99.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 93
ID ACC91399 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 94
ID ACA93495 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003022187-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 95
ID ACD02734 standard; cDNA; 766 BP.
DE cDNA encoding human PRO polypeptide #99.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 96
ID ACC87299 standard; cDNA; 766 BP.

DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 97
ID ACC85883 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 98
ID ABX81177 standard; DNA; 766 BP.
DE Novel human secreted or transmembrane protein PRO812 DNA.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 99
ID ACA65371 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #99.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 100
ID ACA94188 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 101
ID ACA97932 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #99.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 102
ID ACA91434 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 103
ID ACA90648 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 104
ID ACD16195 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 105
ID ACD17356 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 106
ID ACC92013 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003040069-A1.

PD 27-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 107
ID ACD02321 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 108
ID ACA74870 standard; cDNA; 766 BP.
DE cDNA encoding human PRO polypeptide #99.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 109
ID ACA91741 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #99.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 110
ID ACA89312 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 111
ID ACA71385 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 112
ID ACC90785 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 113
ID ACA65795 standard; cDNA; 766 BP.
DE cDNA encoding human PRO protein #99.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 114
ID ACA68949 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 115
ID ACA92993 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003017476-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 116
ID ACA94940 standard; cDNA; 766 BP.
DE cDNA encoding human PRO polypeptide #99.
PN US2003017541-A1.

PD 23-JAN-2003.
 Query Match 100.0%; Score 766; DB 8; Length 766;
 Best Local Similarity 100.0%; Pred. No. 5.8e-222;
 RESULT 117
 ID ACD16502 standard; cDNA; 766 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #99.
 PN US2003017543-A1.
 PD 23-JAN-2003.
 Query Match
 Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
 RESULT 118
 ID ACD15581 standard; cDNA; 766 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #99.
 PN US2003036152-A1.
 PD 20-FEB-2003.
 Query Match
 Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
 RESULT 119
 ID ACA98471 standard; cDNA; 766 BP.
 DE Human PRO polynucleotide #24.
 PN US2003027993-A1.
 PD 06-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 766; DB 8; Length 766;
 Best Local Similarity 100.0%; Pred. No. 5.8e-222;
 RESULT 120
 ID ABX17077 standard; cDNA; 766 BP.
 DE Human PRO polynucleotide #73.
 PN US2002123463-A1.
 PD 05-SEP-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 766; DB 8; Length 766;
 Best Local Similarity 100.0%; Pred. No. 5.8e-222;
 RESULT 121
 ID ABX16684 standard; cDNA; 766 BP.
 DE Human cDNA encoding secreted/transmembrane protein #99.
 PN US2002127584-A1.
 PD 12-SEP-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 766; DB 8; Length 766;
 Best Local Similarity 100.0%; Pred. No. 5.8e-222;
 RESULT 122
 ID ACA67932 standard; cDNA; 766 BP.
 DE Novel human secreted and transmembrane protein PRO994 cDNA.
 PN US2002177164-A1.
 PD 28-NOV-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 766; DB 9; Length 766;
 Best Local Similarity 100.0%; Pred. No. 5.8e-222;
 RESULT 123
 ID ACA63396 standard; cDNA; 766 BP.
 DE cDNA encoding human PRO polypeptide #24.
 PN US2003023042-A1.
 PD 30-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 766; DB 9; Length 766;
 Best Local Similarity 100.0%; Pred. No. 5.8e-222;
 RESULT 124
 ID ACA97625 standard; cDNA; 766 BP.
 DE Human PRO polynucleotide #99.
 PN US2003032115-A1.
 PD 13-FEB-2003.
 Query Match
 Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
 RESULT 125
 ID ACA99074 standard; cDNA; 766 BP.
 DE Novel human secreted and transmembrane protein PRO994 cDNA.
 PN US2003032140-A1.
 PD 13-FEB-2003.
 Query Match 100.0%; Score 766; DB 9; Length 766;
 Best Local Similarity 100.0%; Pred. No. 5.8e-222;
 RESULT 126
 ID ACC91706 standard; cDNA; 766 BP.

DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
 PN US2003040076-A1.
 PD 27-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 766; DB 9; Length 766;
 Best Local Similarity 100.0%; Pred. No. 5.8e-222;
 RESULT 127
 ID ACD1117 standard; cDNA; 766 BP.
 DE Novel human secreted and transmembrane protein PRO994 cDNA.
 PN US2003008352-A1.
 PD 09-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 766; DB 9; Length 766;
 Best Local Similarity 100.0%; Pred. No. 5.8e-222;
 RESULT 128
 ID ACD14967 standard; cDNA; 766 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #99.
 PN US2003044922-A1.
 PD 06-MAR-2003.
 Query Match 100.0%; Score 766; DB 9; Length 766;
 Best Local Similarity 100.0%; Pred. No. 5.8e-222;
 RESULT 129
 ID ACA88381 standard; cDNA; 766 BP.
 DE Human secreted and transmembrane polypeptide PRO994 cDNA.
 PN US2002197615-A1.
 PD 26-DEC-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 766; DB 9; Length 766;
 Best Local Similarity 100.0%; Pred. No. 5.8e-222;
 RESULT 130
 ID ACD81888 standard; cDNA; 766 BP.
 DE cDNA encoding human PRO994 polypeptide.
 PN US2003017981-A1.
 PD 23-JAN-2003.
 Query Match 100.0%; Score 766; DB 9; Length 766;
 Best Local Similarity 100.0%; Pred. No. 5.8e-222;
 RESULT 131
 ID ACD11731 standard; cDNA; 766 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #99.
 PN US2003032118-A1.
 PD 13-FEB-2003.
 Query Match 100.0%; Score 766; DB 9; Length 766;
 Best Local Similarity 100.0%; Pred. No. 5.8e-222;
 RESULT 132
 ID ACC95860 standard; cDNA; 766 BP.
 DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
 PN US2003036135-A1.
 PD 20-FEB-2003.
 Query Match 100.0%; Score 766; DB 9; Length 766;
 Best Local Similarity 100.0%; Pred. No. 5.8e-222;
 RESULT 133
 ID ACF16423 standard; cDNA; 766 BP.
 DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
 PN US2003054455-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 766; DB 9; Length 766;
 Best Local Similarity 100.0%; Pred. No. 5.8e-222;
 RESULT 134
 ID ACF02541 standard; cDNA; 766 BP.
 DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
 PN US2003049741-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 766; DB 9; Length 766;
 Best Local Similarity 100.0%; Pred. No. 5.8e-222;
 RESULT 135
 ID ACF02848 standard; cDNA; 766 BP.
 DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
 PN US2003049743-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 766; DB 9; Length 766;
 Best Local Similarity 100.0%; Pred. No. 5.8e-222;

Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 136
ID ACF21435 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 137
ID ACF10119 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 138
ID ACF78012 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 139
ID ACD46717 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 140
ID ACD49480 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 141
ID ACF28247 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 142
ID ACD89937 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 143
ID ACD84332 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #99.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 144
ID ACD99106 standard; cDNA; 766 BP.
DE cDNA encoding human PRO polypeptide #99.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;

RESULT 145
ID ADA77949 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 146
ID ACF48848 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003104539-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 147
ID ACD09168 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003036131-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 148
ID ACF11961 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003040075-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 149
ID ACF41195 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 150
ID ACF15809 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003044930-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 151
ID ACF16116 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 152
ID ADB17104 standard; cDNA; 766 BP.
DE Human cDNA clone (SeqID 47) encoding the transmembrane PRO protein.
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 153
ID ACD31943 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 154
ID ACF18751 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003064452-A1.
PD 03-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 155
ID ACF09198 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 156
ID ACF78319 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 157
ID ACF51918 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003064440-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 158
ID ACF26405 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 159
ID ACF24198 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 160
ID ACF63509 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 161
ID ACF50383 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 162
ID ACH07854 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 163
ID ACF13660 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;

Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 164
ID ACD41586 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 165
ID ADA37768 standard; cDNA; 766 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO994.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 166
ID ACF31999 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 167
ID ACF23277 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 168
ID ACF39967 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 169
ID ACD45489 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 170
ID ACF53146 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 171
ID ACF27326 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 172
ID ACF45164 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;

RESULT 173
ID ACF29782 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 174
ID ACD89858 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003068635-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 175
ID ACD84639 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #99.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 176
ID ACD98799 standard; cDNA; 766 BP.
DE cDNA encoding human PRO polypeptide #99.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 177
ID ACF77091 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003082717-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 178
ID ACF76784 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 179
ID ACF49769 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003104542-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 180
ID ACF50076 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003104543-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 181
ID ADA21454 standard; cDNA; 766 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO994.
PN US2003054404-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 182
ID ACD09475 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003036127-A1.
PD 20-FEB-2003.

Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 183
ID ACD08554 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003040061-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 184
ID ACH03599 standard; cDNA; 766 BP.
DE Human secreted/transmembrane polypeptide PRO 994 cDNA.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 185
ID ACF12268 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003036130-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 186
ID ACC94776 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 187
ID ACD22495 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 188
ID ACF15195 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003044917-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 189
ID ACC97290 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003044929-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 190
ID ACC92320 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 191
ID ACF13967 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 192
ID ACF14274 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.

PA US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 193
ID ADA10241 standard; cDNA; 766 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO994.
PN US2003059831-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 194
ID ACF09505 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 195
ID ACD45796 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 196
ID ACD47945 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 197
ID ACD67676 standard; cDNA; 766 BP.
DE cDNA encoding human PRO polypeptide #99.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 198
ID ACF25484 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 199
ID ACF29168 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 200
ID ACD84946 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 201
ID ACD84025 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #99.
PN US2003068758-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 202
ID ACD88016 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 203
ID ACF30703 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 204
ID ACF32306 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 205
ID ACH11966 standard; cDNA; 766 BP.
DE cDNA encoding human PRO polypeptide #99.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 206
ID ACH12273 standard; cDNA; 766 BP.
DE cDNA encoding human PRO polypeptide #99.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 207
ID ADA19909 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 208
ID ACD40665 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003032134-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 209
ID ADB17292 standard; cDNA; 766 BP.
DE Human cDNA clone (SeqID 47) encoding the transmembrane PRO protein.
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 210
ID ADA17785 standard; cDNA; 766 BP.
DE cDNA encoding human PRO994 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;

RESULT 211
ID ACF18137 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 212
ID ACF08584 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 213
ID ACF31385 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 214
ID ACF52225 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 215
ID ACD50094 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 216
ID ACF38797 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 217
ID ACF26712 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 218
ID ACF24812 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 219
ID ACF46392 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 220

ID ACF27940 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 221
ID ACD89244 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 222
ID ACF63816 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 223
ID ACF60456 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003087374-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 224
ID ACH12580 standard; cDNA; 766 BP.
DE cDNA encoding human PRO polypeptide #99.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 225
ID ACH10003 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 226
ID ACD03858 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003040055-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 227
ID ACD10396 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003036164-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 228
ID ACD12038 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003040074-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 229
ID ACF42423 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 230
ID ADA27893 standard; cDNA; 766 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO994.
PN US2003054359-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 231
ID ACF18444 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 232
ID ACF02234 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 233
ID ACF21742 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 234
ID ACF10426 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003073169-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 235
ID ACF33878 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 236
ID ACF44840 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 237
ID ACD90472 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 238
ID ACD91085 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 239

ID ACF30396 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 240
ID ACD87095 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 241
ID ACF60149 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 242
ID ACF4699 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003087373-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 243
ID ACF75556 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003096353-A1.
PD 22-MAY-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 244
ID ADA79741 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003073173-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 245
ID ACF17216 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003054458-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 246
ID ACF22970 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 247
ID ACF07970 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 248
ID ACF08277 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 249
ID ACF40581 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 250
ID ACF53760 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 251
ID ACD47024 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 252
ID ACF47927 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 253
ID ACF47313 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 254
ID ACF46085 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 255
ID ACD86174 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 256
ID ACF52532 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003082715-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 257
ID ACF52839 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003082716-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 258

ID ACF64832 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 259
ID ACF76477 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 260
ID ACF61377 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 261
ID ACF61684 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 262
ID ACD30715 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003032125-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 263
ID ACD31636 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003054454-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 264
ID ACD32557 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 265
ID ADA20081 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 266
ID ACD82113 standard; cDNA; 766 BP.
DE Human secreted/transmembrane polypeptide PRO 994 cDNA.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 267
ID ACF17523 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003054460-A1.

PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 268
ID ADA94473 standard; cDNA; 766 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO994.
PN US2003059832-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 269
ID ACF07356 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 270
ID ACF20514 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 271
ID ACF20821 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 272
ID ACF21128 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 273
ID ACD47638 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 274
ID ACF47620 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 275
ID ACF53453 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 276
ID ACD86788 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;

RESULT 277
ID ACH05036 standard; cDNA; 766 BP.
DE cDNA encoding human PRO polypeptide #99.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 278
ID ACF44533 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 279
ID ADA81468 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 280
ID ACD22188 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003027276-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 281
ID ACD24535 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003044920-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 282
ID ACD39738 standard; cDNA; 766 BP.
DE cDNA encoding human PRO polypeptide #99.
PN US2003027265-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 283
ID ACD40045 standard; cDNA; 766 BP.
DE cDNA encoding human PRO polypeptide #99.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 284
ID ACF13353 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 285
ID ACF03155 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 286
ID ACF78626 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003049783-A1.

PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 287
ID ACF11347 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003073171-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 288
ID ACF50690 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003032121-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 289
ID ACF34185 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 290
ID ACD46410 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 291
ID ACD48252 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 292
ID ACF27633 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 293
ID ACF24505 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 294
ID ACD8560 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 295
ID ACD90165 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 296
ID ACD83718 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #99.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 297
ID ACF49155 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003104540-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 298
ID ACH07240 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 299
ID ACH07547 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 300
ID ACH08161 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 301
ID ACH11352 standard; cDNA; 766 BP.
DE cDNA encoding human PRO polypeptide #99.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 302
ID ACH1659 standard; cDNA; 766 BP.
DE cDNA encoding human PRO polypeptide #99.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 303
ID ACH10310 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 304
ID ACF01313 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003040059-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 305
ID ACF40888 standard; cDNA; 766 BP.

DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003040078-A1.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
PD 27-FEB-2003.
RESULT 306
ID ACD24228 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003044918-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
PD 13-FEB-2003.
RESULT 307
ID ACD31329 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003032132-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
PD 20-MAR-2003.
RESULT 308
ID ACF17830 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
PD 27-MAR-2003.
RESULT 309
ID ADA38698 standard; cDNA; 766 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO994.
PN US2003059780-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
PD 27-MAR-2003.
RESULT 310
ID ACF32613 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
PD 03-APR-2003.
RESULT 311
ID ACF40274 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
PD 03-APR-2003.
RESULT 312
ID ACF48234 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003064441-A1.
PD 03-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
PD 03-APR-2003.
RESULT 313
ID ACF38183 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
PD 10-APR-2003.
RESULT 314
ID ACF25119 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
PD 10-APR-2003.

Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 315
ID ACF27019 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
PD 17-APR-2003.
RESULT 316
ID ACF29475 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003073174-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
PD 17-APR-2003.
RESULT 317
ID ACD87709 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
PD 10-APR-2003.
RESULT 318
ID ACF76170 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
PD 05-JUN-2003.
RESULT 319
ID ACF49462 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003104541-A1.
PD 05-JUN-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
PD 05-JUN-2003.
RESULT 320
ID ACF43919 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
PD 05-JUN-2003.
RESULT 321
ID ACH06264 standard; cDNA; 766 BP.
DE cDNA encoding human PRO polypeptide #99.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
PD 13-MAR-2003.
RESULT 322
ID ACH06571 standard; cDNA; 766 BP.
DE cDNA encoding human PRO polypeptide #99.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
PD 13-MAR-2003.
RESULT 323
ID ADA83266 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
PD 13-MAR-2003.
RESULT 324
ID ACC92627 standard; cDNA; 766 BP.

DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003032133-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 325
ID ACC93241 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003032136-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 326
ID ACF19286 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003036129-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 327
ID ACD12977 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003040053-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 328
ID ACF06435 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003040057-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 329
ID ACC94469 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 330
ID ACC97897 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003044932-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 331
ID ACC94162 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003027270-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 332
ID ACF42116 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 333
ID ACD31022 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003032126-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 334
ID ACD43051 standard; cDNA; 766 BP.
DE cDNA encoding human PRO polypeptide #99.

PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 335
ID ACD43358 standard; cDNA; 766 BP.
DE cDNA encoding human PRO polypeptide #99.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 336
ID ACF14888 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 337
ID ADA92819 standard; cDNA; 766 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO994.
PN US2003060407-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 338
ID ACF01620 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003049738-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 339
ID ACF31692 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 340
ID ACD67369 standard; cDNA; 766 BP.
DE cDNA encoding human PRO polypeptide #99.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 341
ID ACD48559 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 342
ID ACD48866 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 343
ID ACF51304 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 344
ID ACF54067 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 345
ID ACF25791 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 346
ID ACF39104 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 347
ID ACF28861 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 348
ID ACD90778 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 349
ID ACD86481 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 350
ID ACH05343 standard; cDNA; 766 BP.
DE cDNA encoding human PRO polypeptide #99.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 351
ID ACF65139 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 352
ID ADB20309 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003082767-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;

RESULT 353
ID ACF43612 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 354
ID ACH09082 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 355
ID ACH09389 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 356
ID ADA78561 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 357
ID ACF09812 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 358
ID ADA00378 standard; cDNA; 766 BP.
DE Human secreted/transmembrane polypeptide PRO 994 cDNA.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 359
ID ACF50997 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 360
ID ACF23891 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 361
ID ACD88323 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 362

ID ACH09696 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 363
ID ACH10617 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 364
ID ACD11424 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003036126-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 365
ID ACC96474 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003044924-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 366
ID ACC98504 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003044927-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 367
ID ACF41809 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003040072-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 368
ID ACF16730 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003040073-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 369
ID ACD32250 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 370
ID ACD30408 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003032124-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 371
ID ACD41279 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;

RESULT 372
ID ACF07663 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 373
ID ACF31078 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 374
ID ACF77398 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 375
ID ACF11040 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003073170-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 376
ID ACF32920 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 377
ID ACF26098 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 378
ID ACD83411 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #99.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 379
ID ACF23584 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 380
ID ACF42998 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 381
ID ACF43305 standard; cDNA; 766 BP.

DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 382
ID ACH05957 standard; cDNA; 766 BP.
DE cDNA encoding human PRO polypeptide #99.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 383
ID ACH08775 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 384
ID ACH90369 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003027273-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 385
ID ACF10733 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003036119-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 386
ID ACC93548 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003036120-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 387
ID ACC96167 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 388
ID ACD24842 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003044921-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 389
ID ACF01927 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 390
ID ACF22049 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;

Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 391
ID ACF22663 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 392
ID ACF08891 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003086887-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 393
ID ACF33227 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 394
ID ACF54681 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 395
ID ACF48541 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003084444-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 396
ID ACD47331 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003086897-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 397
ID ACD49173 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 398
ID ACF37876 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003086886-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 399
ID ACF30089 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;

RESULT 400
ID ACD87402 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 401
ID ACF61991 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003104538-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 402
ID ACHI0924 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 403
ID ACD10089 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003036158-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 404
ID ACD16814 standard; cDNA; 766 BP.
DE cDNA encoding human PRO polypeptide #99.
PN US2003036151-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 405
ID ACH65449 standard; cDNA; 766 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO994.
PN US2003044806-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 406
ID ACC99111 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003040067-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 407
ID ACF00505 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003054456-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 408
ID ACD40972 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 409
ID ACF14581 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 410
ID ACF22356 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 411
ID ACF78933 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 412
ID ACF11654 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 413
ID ADA22380 standard; cDNA; 766 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO994.
PN US2003040473-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 414
ID ACF51611 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 415
ID ACF33534 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 416
ID ACD49787 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 417
ID ACF37569 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068683-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 418
ID ACF28554 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 419
ID ACD88630 standard; cDNA; 766 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003068681-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
Pred. No. 5.8e-222;
RESULT 420
ID ACF75249 standard; cDNA: 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
Pred. No. 5.8e-222;
RESULT 421
ID ACF61070 standard; cDNA: 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
Pred. No. 5.8e-222;
RESULT 422
ID ACF44226 standard; cDNA: 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
Pred. No. 5.8e-222;
RESULT 423
ID ACH08468 standard; cDNA: 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
Pred. No. 5.8e-222;
RESULT 424
ID ACD39439 standard; cDNA: 766 BP.
DE Human cDNA encoding PRO812.
PN US2003017982-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
Pred. No. 5.8e-222;
RESULT 425
ID ACC93855 standard; cDNA: 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003036122-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
Pred. No. 5.8e-222;
RESULT 426
ID ACD20960 standard; cDNA: 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
Pred. No. 5.8e-222;
RESULT 427
ID ACF06742 standard; cDNA: 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003040065-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
Pred. No. 5.8e-222;
RESULT 428
ID ACD20653 standard; cDNA: 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003044919-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
Pred. No. 5.8e-222;

RESULT 429
ID ACD2802 standard; cDNA: 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003040077-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
Pred. No. 5.8e-222;
RESULT 430
ID ACF41502 standard; cDNA: 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003044928-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
Pred. No. 5.8e-222;
RESULT 431
ID ADA06546 standard; cDNA: 766 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #73.
PN US2003049638-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
Pred. No. 5.8e-222;
RESULT 432
ID ADA39239 standard; cDNA: 766 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO994.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
Pred. No. 5.8e-222;
RESULT 433
ID ACF07049 standard; cDNA: 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
Pred. No. 5.8e-222;
RESULT 434
ID ACF77705 standard; cDNA: 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
Pred. No. 5.8e-222;
RESULT 435
ID ACD46103 standard; cDNA: 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
Pred. No. 5.8e-222;
RESULT 436
ID ACF54374 standard; cDNA: 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
Pred. No. 5.8e-222;
RESULT 437
ID ACF54374 standard; cDNA: 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
Pred. No. 5.8e-222;
RESULT 438
ID ACF45778 standard; cDNA: 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068741-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 766; DB 9; Length 766;
 Best Local Similarity 100.0%; Pred. No. 5.8e-222;
 RESULT 439
 ID ACF45471 standard; cDNA; 766 BP.
 DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
 PN US2003068744-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 766; DB 9; Length 766;
 Best Local Similarity 100.0%; Pred. No. 5.8e-222;
 RESULT 440
 ID ACF38490 standard; cDNA; 766 BP.
 DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
 PN US2003068766-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 766; DB 9; Length 766;
 Best Local Similarity 100.0%; Pred. No. 5.8e-222;
 RESULT 441
 ID ACD89551 standard; cDNA; 766 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #99.
 PN US2003068694-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 766; DB 9; Length 766;
 Best Local Similarity 100.0%; Pred. No. 5.8e-222;
 RESULT 442
 ID ACD85253 standard; cDNA; 766 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #99.
 PN US2003068715-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 766; DB 9; Length 766;
 Best Local Similarity 100.0%; Pred. No. 5.8e-222;
 RESULT 443
 ID ACD85867 standard; cDNA; 766 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #99.
 PN US2003068726-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 766; DB 9; Length 766;
 Best Local Similarity 100.0%; Pred. No. 5.8e-222;
 RESULT 444
 ID ACF75863 standard; cDNA; 766 BP.
 DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
 PN US2003104544-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 766; DB 9; Length 766;
 Best Local Similarity 100.0%; Pred. No. 5.8e-222;
 RESULT 445
 ID ACF60763 standard; cDNA; 766 BP.
 DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
 PN US2003096357-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 766; DB 9; Length 766;
 Best Local Similarity 100.0%; Pred. No. 5.8e-222;
 RESULT 446
 ID ACH05650 standard; cDNA; 766 BP.
 DE cDNA encoding human PRO polypeptide #99.
 PN US2003049760-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 766; DB 9; Length 766;
 Best Local Similarity 100.0%; Pred. No. 5.8e-222;
 RESULT 447
 ID ADA82632 standard; cDNA; 766 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #99.
 PN US2003049755-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 766; DB 9; Length 766;
 Best Local Similarity 100.0%; Pred. No. 5.8e-222;
 RESULT 448
 ID ADB85620 standard; cDNA; 766 BP.
 DE Novel human secreted and transmembrane protein PRO994 cDNA.
 PN US2003049735-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 766; DB 9; Length 766;
 Best Local Similarity 100.0%; Pred. No. 5.8e-222;
 RESULT 449
 ID ADB96265 standard; cDNA; 766 BP.
 DE Human PRO polynucleotide #73.
 PN US2003054403-A1.
 PD 20-MAR-2003.
 Query Match 100.0%; Score 766; DB 9; Length 766;
 Best Local Similarity 100.0%; Pred. No. 5.8e-222;
 RESULT 450
 ID ACF55909 standard; cDNA; 766 BP.
 DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
 PN US2003068680-A1.
 PD 10-APR-2003.
 Query Match 100.0%; Score 766; DB 9; Length 766;
 Best Local Similarity 100.0%; Pred. No. 5.8e-222;
 RESULT 451
 ID ACF55295 standard; cDNA; 766 BP.
 DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
 PN US2003068762-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 766; DB 10; Length 766;
 Best Local Similarity 100.0%; Pred. No. 5.8e-222;
 RESULT 452
 ID ADB85940 standard; cDNA; 766 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #99.
 PN US2003054472-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 766; DB 10; Length 766;
 Best Local Similarity 100.0%; Pred. No. 5.8e-222;
 RESULT 453
 ID ACF56216 standard; cDNA; 766 BP.
 DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
 PN US2003068708-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 766; DB 10; Length 766;
 Best Local Similarity 100.0%; Pred. No. 5.8e-222;
 RESULT 454
 ID ACF56523 standard; cDNA; 766 BP.
 DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
 PN US2003068713-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 766; DB 10; Length 766;
 Best Local Similarity 100.0%; Pred. No. 5.8e-222;
 RESULT 455
 ID ADB68299 standard; cDNA; 766 BP.
 DE Human PRO994 cDNA.
 PN US20030685161-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 766; DB 10; Length 766;
 Best Local Similarity 100.0%; Pred. No. 5.8e-222;
 RESULT 456
 ID ADB68106 standard; cDNA; 766 BP.
 DE Human PRO994 cDNA.
 PN US2003060600-A1.
 PD 27-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 766; DB 10; Length 766;
 Best Local Similarity 100.0%; Pred. No. 5.8e-222;
 RESULT 457

ID ACF55602 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 458
ID ACF54988 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 459
ID ADB90923 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 460
ID ADC57737 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #73.
PN US2003027754-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 461
ID ADC55101 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #73.
PN US2003045463-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 462
ID ADC11968 standard; cDNA; 766 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO994.
PN US2003049681-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 463
ID ADC07003 standard; cDNA; 766 BP.
DE Human PRO994 cDNA.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 464
ID ADC56390 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #73.
PN US2003064375-A1.
PD 03-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 465
ID ADC17182 standard; cDNA; 766 BP.
DE cDNA sequence encoding a PRO polypeptide (SeqID 47).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 466
ID ADC07445 standard; cDNA; 766 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO994.
PN US2003068647-A1.
PD 10-APR-2003.
Query Match
100.0%; Score 766; DB 10; Length 766;

Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 467
ID ADC11435 standard; cDNA; 766 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO994.
PN US2003069403-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 468
ID ADC14880 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 469
ID ADC52375 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 470
ID ADC14557 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003082546-A1.
PD 01-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 471
ID ADD08089 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003068623-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 472
ID ADC81914 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #73.
PN US2003083461-A1.
PD 01-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 473
ID ADD07556 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 474
ID ADC82447 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #73.
PN US2003059833-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 475
ID ADD05670 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 476
ID ADD08627 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003073090-A1.
PD 17-APR-2003.

Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 477
ID ADD06876 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 478
ID ADC83123 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #73.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 479
ID ADD55230 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #73.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 480
ID ADD36051 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 481
ID ADD56188 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #73.
PN US2003077594-A1.
PD 24-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 482
ID ADD54626 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #73.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 483
ID ADE26780 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003087304-A1.
PD 08-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 484
ID ADE26247 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 485
ID ADF67184 standard; cDNA; 766 BP.
DE Human PRO994 nucleotide sequence SEQ ID NO:257.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 486
ID AG01052 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003078387-A1.

PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 487
ID ADG08605 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 488
ID ADG02665 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 489
ID ADG01372 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 490
ID ADF95547 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 491
ID ADF95226 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 492
ID ADG12362 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003207392-A1.
PD 06-NOV-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 493
ID ADH24079 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 494
ID ADH34105 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 495
ID ADH29938 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 496
ID ADH23909 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180919-A1.
PD 25-SEP-2003
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 497
ID ADH09022 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #99.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 498
ID ADH85313 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 499
ID ADH24589 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 500
ID ADH37445 standard; cDNA; 766 BP.
DE Human secreted and transmembrane protein PRO994 cDNA.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 501
ID ADH02034 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #24.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 502
ID ADH37615 standard; cDNA; 766 BP.
DE Human secreted and transmembrane protein PRO994 cDNA.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 503
ID ADH85653 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 504
ID ADH24249 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;

Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 505
ID ADH38543 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181643-A1.
PD 25-SEP-2003
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 506
ID ADH83664 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #24.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 507
ID ADH29472 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 508
ID ADH27588 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 509
ID ADH37785 standard; cDNA; 766 BP.
DE Human secreted and transmembrane protein PRO994 cDNA.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 510
ID ADH37962 standard; cDNA; 766 BP.
DE Human secreted and transmembrane protein PRO994 cDNA.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 511
ID ADH57382 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 512
ID ADH53524 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 513
ID ADH53694 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;

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RESULT 514
ID ADH52030 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
Pred. No. 5.8e-222;
RESULT 515
ID ADH49885 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
Pred. No. 5.8e-222;
RESULT 516
ID ADI23195 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
Pred. No. 5.8e-222;
RESULT 517
ID ADH90188 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
Pred. No. 5.8e-222;
RESULT 518
ID ADI25565 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
Pred. No. 5.8e-222;
RESULT 519
ID ADH97739 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
Pred. No. 5.8e-222;
RESULT 520
ID ADI35438 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #73.
PN US2003050457-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
Pred. No. 5.8e-222;
RESULT 521
ID ADI03587 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
Pred. No. 5.8e-222;
RESULT 522
ID ADI11944 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #24.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
Pred. No. 5.8e-222;
RESULT 523
ID ADH90018 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003032127-A1.
PD 13-FEB-2003.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
Pred. No. 5.8e-222;
RESULT 524
ID ADH99930 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003049682-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
Pred. No. 5.8e-222;
RESULT 525
ID ADH98419 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
Pred. No. 5.8e-222;
RESULT 526
ID ADI11094 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #24.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
Pred. No. 5.8e-222;
RESULT 527
ID ADI11604 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #24.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
Pred. No. 5.8e-222;
RESULT 528
ID ADH98249 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
Pred. No. 5.8e-222;
RESULT 529
ID ADH98589 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
Pred. No. 5.8e-222;
RESULT 530
ID ADH98079 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
Pred. No. 5.8e-222;
RESULT 531
ID ABX78626 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #99.
PN US2003027272-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
Pred. No. 5.8e-222;
RESULT 532
ID ACA75598 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003032127-A1.
PD 13-FEB-2003.
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Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 533
ID ACA71078 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003032112-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 534
ID ACC87606 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003027278-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 535
ID ACC86992 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003036159-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 536
ID ACD04165 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003040070-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 537
ID ABX77878 standard; cDNA; 766 BP.
DE Novel human secreted or transmembrane protein PRO812 DNA.
PN US2002132252-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 539
ID ACA69196 standard; cDNA; 766 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO994.
PN US2003032023-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 540
ID ACA69496 standard; cDNA; 766 BP.
DE cDNA encoding human PRO polypeptide #99.
PN US2003032113-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 541
ID ACA90341 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003036147-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 542
ID ACC89448 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;

RESULT 543
ID ABX90267 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein cDNA, #103.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 544
ID ACA98239 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 545
ID ACA93881 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 546
ID ACD15274 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 547
ID ACD08861 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 548
ID ACC96781 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 549
ID ACF15502 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 550
ID ABX64113 standard; cDNA; 766 BP.
DE cDNA encoding human PRO994 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 551
ID ACA72869 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #99.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 552
ID ACD03041 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;

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RESULT 553
ID AC001856 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 554
ID ACA92048 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 555
ID ADI05067 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 556
ID ADI03417 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 557
ID ADI04812 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 558
ID ADH78266 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #24.
PN US2003181668-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 559
ID ADI19610 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 560
ID ADH90358 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 561
ID ADI03077 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 562
ID ADH77926 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #24.
PN US2003191290-A1.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 563
ID ADH97909 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 564
ID ADI01294 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 565
ID ADI01989 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 566
ID ADI03247 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 567
ID ADI11434 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #24.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 568
ID ADI02336 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 569
ID ADI11774 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #24.
PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 570
ID ADI05411 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 571
ID ADH79483 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003191290-A1.
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PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 572
ID ADI19440 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 573
ID ADI05241 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 574
ID ADH79653 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 575
ID ADI01479 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 576
ID ADI01649 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 577
ID ADI01819 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 578
ID ADH79823 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 579
ID ADI04641 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 580
ID ADI02777 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181651-A1.
PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 581
ID ADH78096 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #24.
PN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 582
ID ADI25735 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 583
ID ADI25905 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 584
ID ADK65417 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 585
ID ADH98759 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 586
ID ADH80000 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 587
ID ADL32803 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 11; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 588
ID ADM30337 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 11; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 589
ID ADL93731 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 100.0%; Score 766; DB 11; Length 766;
RESULT 590
ID ADC52185 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 12; Length 766;
RESULT 591
ID ADE74334 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003211572-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 12; Length 766;
RESULT 592
ID ADE74946 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003211574-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 12; Length 766;
RESULT 593
ID ADF35383 standard; cDNA; 766 BP.
DE cDNA encoding human PRO994 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 12; Length 766;
RESULT 594
ID ADG11633 standard; cDNA; 766 BP.
DE cDNA encoding human PRO994 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 12; Length 766;
RESULT 595
ID ADF96159 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003215909-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 12; Length 766;
RESULT 596
ID ADG04430 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 12; Length 766;
RESULT 597
ID ADG00590 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 12; Length 766;
RESULT 598
ID ADH06617 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 12; Length 766;
RESULT 599
ID ADH06447 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.

PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 12; Length 766;
RESULT 600
ID ADG68868 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 12; Length 766;
RESULT 601
ID ADH27758 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 12; Length 766;
RESULT 602
ID ADH25099 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 12; Length 766;
RESULT 603
ID ADH33731 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #24.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 12; Length 766;
RESULT 604
ID ADG82846 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #99.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 12; Length 766;
RESULT 605
ID ADH02374 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #24.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 12; Length 766;
RESULT 606
ID ADH07981 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 12; Length 766;
RESULT 607
ID ADG69378 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 12; Length 766;
RESULT 608
ID ADH39199 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180917-A1.

PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 609
ID ADH26127 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 610
ID ADG83939 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #24.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 611
ID ADH19503 standard; cDNA; 766 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO994.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 612
ID ADG85483 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 613
ID ADH06277 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 614
ID ADH30107 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 615
ID ADH24419 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 616
ID ADH33096 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #99.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 617
ID ADG69548 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180844-A1.
PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 618
ID ADH07811 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 619
ID ADG85823 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 620
ID ADH39369 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 621
ID ADH33561 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #24.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 622
ID ADH33901 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #24.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 623
ID ADH01111 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #24.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 624
ID ADG69718 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 625
ID ADH20996 standard; cDNA; 766 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO994.
PN US2003224358-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 626
ID ADH02204 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #24.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;

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Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 627
ID ADG69208 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
FN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 628
ID ADG85993 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
FN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 629
ID ADH24929 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
FN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 630
ID ADH39546 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
FN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 631
ID ADH20036 standard; cDNA; 766 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO994.
FN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 632
ID ADH02544 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #24.
FN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 633
ID ADG69038 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
FN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 634
ID ADH07641 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
FN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 635
ID ADG86163 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
FN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 636
ID ADH24759 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
FN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 637
ID ADH25807 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
FN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 638
ID ADH38373 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
FN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 639
ID ADH57212 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
FN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 640
ID ADH52200 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
FN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 641
ID ADH49566 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
FN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 642
ID ADH90528 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
FN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 643
ID ADI11264 standard; cDNA; 766 BP.
DE Human PRO Polynucleotide #24.
FN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 644
ID ADH98929 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
FN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 645
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ID ADI02159 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
FN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 646
ID ADH90698 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
FN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 647
ID ADJ54835 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #99.
FN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 648
ID ADJ98573 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
FN US2003181797-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 649
ID ADJ98743 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
FN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 650
ID ADH78902 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
FN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 651
ID ADJ99136 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
FN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 652
ID ADJ99306 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
FN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 653
ID ADJ98924 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
FN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 654
ID ADH79072 standard; cDNA; 766 BP.

DE Novel human secreted and transmembrane protein PRO994 cDNA.
FN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 655
ID ADK00932 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #24.
FN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 656
ID ADK14453 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
FN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 657
ID ADJ64606 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #99.
FN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 658
ID ADM31502 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
FN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 659
ID ADM36549 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
FN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 660
ID ADM40354 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
FN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 661
ID ADM80902 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #24.
FN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 662
ID ADM37962 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
FN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 663
ID AAK88578 standard; cDNA; 734 BP.
DE Human digestive system antigen coding sequence SEQ ID NO: 894.

PN WO200155314-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 56.1%; Score 429.6; DB 4; Length 734;
 Best Local Similarity 98.7%; Pred. No. 9.6e-120;
 RESULT 664
 ID AAS37892 standard; cDNA; 351 BP.
 DE Novel human diagnostic and therapeutic gene #950.
 PN WO200166753-A2.
 PD 13-SEP-2001.
 PA (CHIR) CHIRON CORP.
 PA (HYSE-) HYSEQ INC.
 Query Match 34.5%; Score 264.2; DB 4; Length 351;
 Best Local Similarity 91.0%; Pred. No. 1.2e-69;
 RESULT 665
 ID AAF98695 standard; DNA; 286 BP.
 DE Human ovarian cancer cell expressed sequence 10793.
 PN WO200118542-A2.
 PD 15-MAR-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 30.2%; Score 231.4; DB 5; Length 286;
 Best Local Similarity 99.6%; Pred. No. 1.1e-59;
 RESULT 666
 ID AAS38101 standard; cDNA; 378 BP.
 DE Novel human diagnostic and therapeutic gene #1159.
 PN WO200166753-A2.
 PD 13-SEP-2001.
 PA (CHIR) CHIRON CORP.
 PA (HYSE-) HYSEQ INC.
 Query Match 19.4%; Score 148.6; DB 4; Length 378;
 Best Local Similarity 89.4%; Pred. No. 1.7e-34;
 RESULT 667
 ID ABS72969 standard; cDNA; 106 BP.
 DE Human gene trapped sequence (GTS) #929.
 PN US2002095031-A1.
 PD 18-JUL-2002.
 PA (NEHL/) NEHLS M C.
 PA (ZAMB/) ZAMBROWICZ B.
 PA (SAND/) SANDS A T.
 Query Match 9.0%; Score 69; DB 6; Length 106;
 Best Local Similarity 88.7%; Pred. No. 1.5e-10;
 RESULT 668
 ID ABN47584 standard; DNA; 60 BP.
 DE Human spliced transcript detection oligonucleotide SEQ ID NO:20332.
 PN WO200210449-A2.
 PD 07-FEB-2002.
 PA (COMP-) COMPUGEN INC.
 Query Match 7.8%; Score 60; DB 6; Length 60;
 Best Local Similarity 100.0%; Pred. No. 6.2e-08;
 RESULT 669
 ID ADA71938 standard; DNA; 2000 BP.
 DE Rice gene, SEQ ID 5263.
 PN WO2003000898-A1.
 PD 03-JAN-2003.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Query Match 5.7%; Score 43.4; DB 8; Length 2000;
 Best Local Similarity 10.6%; Pred. No. 0.035;
 RESULT 670
 ID ACH17322 standard; cDNA; 404 BP.
 DE Human adult heart cDNA #1636.
 PN US2003073623-A1.
 PD 17-APR-2003.
 PA (DRMA/) DRMANAC R T.
 PA (LABA/) LABAT I.
 PA (STAC/) STACHE-CRAIN B.
 PA (DICK/) DICKSON M C.
 PA (JONE/) JONES L W.
 Query Match 5.1%; Score 39.4; DB 9; Length 404;
 Best Local Similarity 52.8%; Pred. No. 0.27;
 RESULT 671
 ID ACH15938 standard; cDNA; 410 BP.
 DE Human adult heart cDNA #252.
 PN US2003073623-A1.

PD 17-APR-2003.
 PA (DRMA/) DRMANAC R T.
 PA (LABA/) LABAT I.
 PA (STAC/) STACHE-CRAIN B.
 PA (DICK/) DICKSON M C.
 PA (JONE/) JONES L W.
 Query Match 5.1%; Score 39.4; DB 9; Length 410;
 Best Local Similarity 52.8%; Pred. No. 0.28;
 RESULT 672
 ID ACC44333 standard; DNA; 3447 BP.
 DE Gene encoding human structural and cytoskeletal associated protein #37.
 PN WO2003031940-A2.
 PD 17-APR-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 5.1%; Score 39.4; DB 8; Length 3447;
 Best Local Similarity 52.8%; Pred. No. 0.75;
 RESULT 673
 ID ADD14717 standard; cDNA; 8034 BP.
 DE Human src biomarker polynucleotide SEQ ID NO:111.
 PN WO2003062395-A2.
 PD 31-JUL-2003.
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 Query Match 5.1%; Score 39.4; DB 10; Length 8034;
 Best Local Similarity 52.8%; Pred. No. 1.1;
 RESULT 674
 ID ADI24481 standard; cDNA; 8034 BP.
 DE Human modifier of Chk1 (MCHK) encoding cDNA SEQ ID NO:31.
 PN WO2004004785-A1.
 PD 15-JAN-2004.
 PA (EXEL-) EXELIXIS INC.
 Query Match 5.1%; Score 39.4; DB 12; Length 8034;
 Best Local Similarity 52.8%; Pred. No. 1.1;
 RESULT 675
 ID AAS35237 standard; cDNA; 447 BP.
 DE Human cardiovascular system antigen cDNA polynucleotide SEQ ID NO 122.
 PN WO200155321-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 5.1%; Score 39; DB 4; Length 447;
 Best Local Similarity 52.2%; Pred. No. 0.38;
 RESULT 676
 ID ADE45316 standard; cDNA; 447 BP.
 DE Human cardiovascular system related polynucleotide #112.
 PN US2003059908-A1.
 PD 27-MAR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 5.1%; Score 39; DB 10; Length 447;
 Best Local Similarity 52.2%; Pred. No. 0.38;
 RESULT 677
 ID ADC93538 standard; DNA; 369 BP.
 DE E. faecium DNA sequence SEQ ID 3165.
 PN US6583275-B1.
 PD 24-JUN-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 4.8%; Score 36.4; DB 10; Length 369;
 Best Local Similarity 51.2%; Pred. No. 2.1;
 RESULT 678
 ID ABN26464 standard; cDNA; 427 BP.
 DE Human OREX polynucleotide sequence SEQ ID NO:21405.
 PN WO200192523-A2.
 PD 06-DEC-2001.
 PA (CURA-) CURAGEN CORP.
 Query Match 4.7%; Score 36.2; DB 6; Length 427;
 Best Local Similarity 46.0%; Pred. No. 2.6;
 RESULT 679
 ID AAX13287 standard; DNA; 3274 BP.
 DE Enterococcus faecalis genome contig SEQ ID NO:350.
 PN WO9850555-A2.
 PD 12-NOV-1998.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 4.7%; Score 36.2; DB 2; Length 3274;
 Best Local Similarity 51.6%; Pred. No. 6.8;
 RESULT 680

ID ABS99082 standard; DNA; 3274 BP.
 DE Enterococcus faecalis contig sequence #350.
 PN US2002120116-A1.
 PD 29-AUG-2002.
 PA (KUNS/) KUNSCH C A.
 PA (DILL/) DILLON P J.
 PA (BARA/) BARASH S.
 Query Match
 Best Local Similarity 4.7%; Score 36.2; DB 6; Length 3274;
 Best Local Similarity 51.6%; Pred. No. 6.8;
 RESULT 681
 ID ABL33154 standard; DNA; 5807 BP.
 DE Human immune system associated gene SEQ ID NO: 1127.
 PN WO200200928-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match
 Best Local Similarity 4.7%; Score 36; DB 6; Length 5807;
 Best Local Similarity 64.3%; Pred. No. 10;
 RESULT 682
 ID ABX57335 standard; DNA; 540 BP.
 DE Arabidopsis thaliana polynucleotide #687.
 PN US2002040489-A1.
 PD 04-APR-2002.
 PA (GORL/) GORLACH J.
 PA (ANYV/) AN Y.
 PA (HAML/) HAMILTON C M.
 PA (PRIC/) PRICE J L.
 PA (RAIN/) RAINES T M.
 PA (YUYV/) YU Y.
 PA (RAME/) RAMEAKA J G.
 PA (PAGE/) PAGE A.
 PA (MATH/) MATHIEW A V.
 PA (LEDF/) LEDFORD B L.
 PA (WOES/) WOESSNER J P.
 PA (HAAS/) HAAS W D.
 PA (GARC/) GARCIA C A.
 PA (KRIC/) KRICKER M.
 PA (SLAT/) SLATER T.
 PA (DAVI/) DAVIS K R.
 PA (ALLE/) ALLEN K.
 PA (HOFF/) HOFFMAN N.
 PA (HURB/) HUREAN P.
 Query Match
 Best Local Similarity 4.6%; Score 35; DB 10; Length 540;
 Best Local Similarity 50.9%; Pred. No. 6.8;
 RESULT 683
 ID ADP84152 standard; DNA; 42347 BP.
 DE Human CAL25 genomic DNA extracellular repeat sequence SeqID 2.
 Query Match
 Best Local Similarity 4.6%; Score 35; DB 12; Length 42347;
 Best Local Similarity 49.2%; Pred. No. 53;
 RESULT 684
 ID AAC84840 standard; cDNA; 1809 BP.
 DE Sunflower berberine bridge enzyme (BBE) encoding cDNA.
 PN WO200078983-A2.
 PD 28-DEC-2000.
 PA (PION-) PIONEER HI-BRED INT INC.
 PA (CURA-) CURAGEN CORP.
 Query Match
 Best Local Similarity 4.5%; Score 34.8; DB 5; Length 1809;
 Best Local Similarity 50.6%; Pred. No. 14;
 RESULT 685
 ID AAS86817 standard; cDNA; 2926 BP.
 DE DNA encoding novel human diagnostic protein #22621.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match
 Best Local Similarity 4.5%; Score 34.8; DB 5; Length 2926;
 Best Local Similarity 52.8%; Pred. No. 17;
 RESULT 686
 ID AAS90969 standard; cDNA; 2926 BP.
 DE DNA encoding novel human diagnostic protein #26773.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match
 Best Local Similarity 4.5%; Score 34.8; DB 5; Length 2926;
 Best Local Similarity 52.8%; Pred. No. 17;

RESULT 687
 Query Match
 Best Local Similarity 4.5%; Score 34.8; DB 10; Length 110000;
 Best Local Similarity 55.9%; Pred. No. 94;
 RESULT 688
 ID ACF65382 standard; DNA; 243072 BP.
 DE Photorhabdus luminescens nucleotide sequence #35.
 PN WO200294867-A2.
 PD 28-NOV-2002.
 PA (INSP) INST PASTEUR.
 PA (CNRS) CNRS CENT NAT RECH SCI.
 Query Match
 Best Local Similarity 4.5%; Score 34.8; DB 10; Length 243072;
 Best Local Similarity 55.9%; Pred. No. 1.4e+02;
 RESULT 689
 ID AAX84332 standard; DNA; 5059 BP.
 DE Stealth virus nucleic acid clone, SEQ ID NO: 24.
 Query Match
 Best Local Similarity 4.5%; Score 34.6; DB 2; Length 5059;
 Best Local Similarity 14.2%; Pred. No. 26;
 RESULT 690
 ID ABL32051 standard; DNA; 16545 BP.
 DE Human immune system associated gene SEQ ID NO: 24.
 PN WO200200928-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match
 Best Local Similarity 4.5%; Score 34.6; DB 6; Length 16545;
 Best Local Similarity 47.8%; Pred. No. 45;
 RESULT 691
 ID ABZ32482 standard; DNA; 1413 BP.
 DE Candida albicans essential gene SEQ ID NO 6769.
 PN WO200253728-A2.
 PD 11-JUL-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match
 Best Local Similarity 4.5%; Score 34.4; DB 6; Length 1413;
 Best Local Similarity 50.0%; Pred. No. 16;
 RESULT 692
 ID AAS96692 standard; DNA; 8880 BP.
 DE Arabidopsis DMT2 (IDMT2) DNA.
 PN WO200180626-A1.
 PD 01-NOV-2001.
 PA (REGC) UNIV CALIFORNIA.
 Query Match
 Best Local Similarity 4.5%; Score 34.2; DB 6; Length 8880;
 Best Local Similarity 53.3%; Pred. No. 44;
 RESULT 693
 ID ADM39541 standard; DNA; 8880 BP.
 DE DMT polynucleotide #7.
 PN US2003135890-A1.
 PD 17-JUL-2003.
 PA (FISC/) FISCHER R.
 PA (CHOI/) CHOI Y.
 PA (HANN/) HANNON M.
 PA (OKAM/) OKAMURO J.
 PA (TATA/) TATARINOVA T.
 Query Match
 Best Local Similarity 4.5%; Score 34.2; DB 11; Length 8880;
 Best Local Similarity 53.3%; Pred. No. 44;
 RESULT 694
 ID AAK70445 standard; DNA; 18949 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25257.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match
 Best Local Similarity 4.5%; Score 34.2; DB 4; Length 18949;
 Best Local Similarity 53.6%; Pred. No. 63;
 RESULT 695
 ID AAX20253 standard; DNA; 26811 BP.
 DE Borrelia burgdorferi polynucleotide sequence #6.
 PN WO9858943-A1.
 PD 30-DEC-1998.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (MEDI-) MEDIMMUNE INC.
 Query Match
 Best Local Similarity 4.5%; Score 34.2; DB 2; Length 26811;
 Best Local Similarity 47.9%; Pred. No. 74;
 RESULT 696
 Query Match
 Best Local Similarity 4.5%; Score 34.2; DB 6; Length 110000;
 Best Local Similarity 52.4%; Pred. No. 1.4e+02;

RESULT 697
ID ABO76613 standard; cDNA; 24142 BP.
DE C. albicans BAX-associated cDNA fragment SEQ ID 651.
PN WO200264766-A2.
PD 22-AUG-2002.
PA (JANC-) JANSSEN PHARM NV.
Query Match 4.4%; Score 34; DB 6; Length 24142;
Best Local Similarity 51.3%; Pred. No. 81;
RESULT 698
ID ADO47193 standard; DNA; 200000 BP.
DE DNA sequence of a human immunoglobulin heavy chain variable region.
PN WO2004023249-A1.
PD 08-APR-2004.
PA (CENT-) CENTENARY INST CANCER MEDICINE & CELL BI.
Query Match 4.4%; Score 34; DB 12; Length 200000;
Best Local Similarity 57.5%; Pred. No. 2.2e+02;
RESULT 699
ID AAI18674 standard; DNA; 575 BP.
DE Probe #8607 for gene expression analysis in human cervical cell sample.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 4.4%; Score 33.8; DB 4; Length 575;
Best Local Similarity 55.6%; Pred. No. 16;
RESULT 700
ID ABA63673 standard; DNA; 575 BP.
DE Human foetal liver single exon nucleic acid probe #11978.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 4.4%; Score 33.8; DB 4; Length 575;
Best Local Similarity 55.6%; Pred. No. 16;
RESULT 701
ID AAI43787 standard; DNA; 575 BP.
DE Probe #12473 used to measure gene expression in human placenta sample.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 4.4%; Score 33.8; DB 4; Length 575;
Best Local Similarity 55.6%; Pred. No. 16;
RESULT 702
ID AAK37911 standard; DNA; 575 BP.
DE Human bone marrow expressed single exon probe SEQ ID NO: 12468.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 4.4%; Score 33.8; DB 4; Length 575;
Best Local Similarity 55.6%; Pred. No. 16;
RESULT 703
ID AAK12190 standard; DNA; 575 BP.
DE Human brain expressed single exon probe SEQ ID NO: 12181.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 4.4%; Score 33.8; DB 4; Length 575;
Best Local Similarity 55.6%; Pred. No. 16;
RESULT 704
ID ABS37535 standard; DNA; 575 BP.
DE Human liver single exon probe, SEQ ID NO 12525.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 4.4%; Score 33.8; DB 4; Length 575;
Best Local Similarity 55.6%; Pred. No. 16;
RESULT 705
ID ABS11910 standard; DNA; 575 BP.
DE Human genome-derived single exon probe from lung SEQ ID NO 11901.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 4.4%; Score 33.8; DB 6; Length 575;
Best Local Similarity 55.6%; Pred. No. 16;
RESULT 706
ID AAK37911 standard; DNA; 575 BP.
DE Human bone marrow expressed single exon probe SEQ ID NO: 12468.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 4.4%; Score 33.8; DB 4; Length 575;
Best Local Similarity 55.6%; Pred. No. 16;

ID ACC00411 standard; cDNA; 1088 BP.
DE Human cell adhesion and extracellular matrix protein, CADECM-20, DNA.
PN WO2003027230-A2.
PD 03-APR-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 4.4%; Score 33.6; DB 8; Length 1088;
Best Local Similarity 63.8%; Pred. No. 25;
RESULT 707
ID ABO67033 standard; DNA; 17970 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 63.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.4%; Score 33.6; DB 6; Length 17970;
Best Local Similarity 44.8%; Pred. No. 94;
RESULT 708
Query Match 4.4%; Score 33.6; DB 6; Length 110000;
Best Local Similarity 49.4%; Pred. No. 2.2e+02;
RESULT 709
ID ADL13512 standard; DNA; 178870 BP.
DE Osteoarthritis-associated polymorphic nucleotide #44.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 4.4%; Score 33.6; DB 10; Length 178870;
Best Local Similarity 55.0%; Pred. No. 2.7e+02;
RESULT 710
ID ABN67938 standard; DNA; 912 BP.
DE Streptococcus polynucleotide SEQ ID NO 3789.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 4.4%; Score 33.4; DB 6; Length 912;
Best Local Similarity 53.4%; Pred. No. 27;
RESULT 711
ID AAS61095 standard; DNA; 5375 BP.
DE Human gene regulation-associated gene oligonucleotide #50.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.4%; Score 33.4; DB 6; Length 5975;
Best Local Similarity 53.4%; Pred. No. 64;
RESULT 712
ID AAS46550 standard; DNA; 6558 BP.
DE Tumour suppressor gene derived chemically modified sequence #272.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.4%; Score 33.4; DB 4; Length 6558;
Best Local Similarity 48.7%; Pred. No. 67;
RESULT 713
ID ADB54160 standard; DNA; 6558 BP.
DE Pretreated genomic DNA region 84.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.4%; Score 33.4; DB 10; Length 6558;
Best Local Similarity 48.7%; Pred. No. 67;
RESULT 714
ID ADB54288 standard; DNA; 6558 BP.
DE Pretreated genomic DNA region 212.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.4%; Score 33.4; DB 10; Length 6558;
Best Local Similarity 48.7%; Pred. No. 67;
RESULT 715
ID ADC87618 standard; DNA; 58366 BP.
DE Human GPCR related polynucleotide SEQ ID NO:2071.
PN EPI270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
 Query Match 4.4%; Score 33.4; DB 10; Length 58366;
 Best Local Similarity 47.0%; Pred. No. 1.9e+02;
 RESULT 716
 ID AAH15410 standard; cDNA; 1391 BP.
 DE Human cDNA sequence SEQ ID NO:13620.
 PN EP1074617-A2.
 PD 07-FEB-2001.
 PA (HBLI-) HELIX RES INST.
 Query Match 4.3%; Score 33; DB 4; Length 1391;
 Best Local Similarity 51.7%; Pred. No. 43;
 RESULT 717
 ID AB213052 standard; DNA; 1602 BP.
 DE Arabidopsis thaliana stress regulated gene SEQ ID NO 857.
 PN WO200216655-A2.
 PD 28-FEB-2002.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Query Match 4.3%; Score 33; DB 6; Length 1602;
 Best Local Similarity 49.2%; Pred. No. 46;
 RESULT 718
 ID AAC46279 standard; DNA; 1971 BP.
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 49562.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Query Match 4.3%; Score 33; DB 3; Length 1971;
 Best Local Similarity 49.2%; Pred. No. 51;
 RESULT 719
 ID ADA71938 standard; DNA; 2000 BP.
 DE Rice gene. SEQ ID 5263.
 PN WO200300898-A1.
 PD 03-JAN-2003.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Query Match 4.3%; Score 33; DB 8; Length 2000;
 Best Local Similarity 9.2%; Pred. No. 51;
 RESULT 720
 ID ADP6597 standard; DNA; 2001 BP.
 DE Human, Similar to collagen, type V, alpha 2, clone DNA.
 PN WO2003072827-A1.
 PD 04-SEP-2003.
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
 Query Match 4.3%; Score 33; DB 11; Length 2001;
 Best Local Similarity 45.5%; Pred. No. 51;
 RESULT 721
 ID ADP65797 standard; DNA; 2001 BP.
 DE Human, Similar to collagen, type V, alpha 2, clone DNA.
 PN WO2003072827-A1.
 PD 04-SEP-2003.
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
 Query Match 4.3%; Score 33; DB 11; Length 2001;
 Best Local Similarity 45.5%; Pred. No. 51;
 RESULT 722
 ID AAH54098 standard; DNA; 3103 BP.
 DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:3462.
 PN WO200134809-A2.
 PD 17-MAY-2001.
 PA (GLAX) GLAXO GROUP LTD.
 Query Match 4.3%; Score 33; DB 4; Length 3103;
 Best Local Similarity 55.8%; Pred. No. 63;
 RESULT 723
 ID AAH54877 standard; DNA; 3438 BP.
 DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:4241.
 PN WO200134809-A2.
 PD 17-MAY-2001.
 PA (GLAX) GLAXO GROUP LTD.
 Query Match 4.3%; Score 33; DB 4; Length 3438;
 Best Local Similarity 55.8%; Pred. No. 66;
 RESULT 724
 ID AAH54633 standard; DNA; 3463 BP.
 DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:3997.
 PN WO200134809-A2.
 PD 17-MAY-2001.
 PA (GLAX) GLAXO GROUP LTD.

Query Match 4.3%; Score 33; DB 4; Length 3463;
 Best Local Similarity 55.8%; Pred. No. 66;
 RESULT 725
 ID ADP65055 standard; DNA; 6217 BP.
 DE Human collagen, type V, alpha 2 (COL5A2) DNA sequence.
 PN WO2003072827-A1.
 PD 04-SEP-2003.
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
 Query Match 4.3%; Score 33; DB 11; Length 6217;
 Best Local Similarity 45.5%; Pred. No. 87;
 RESULT 726
 ID ADP65717 standard; DNA; 6217 BP.
 DE Human collagen, type V, alpha 2 (COL5A2) DNA.
 PN WO2003072827-A1.
 PD 04-SEP-2003.
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
 Query Match 4.3%; Score 33; DB 11; Length 6217;
 Best Local Similarity 45.5%; Pred. No. 87;
 RESULT 727
 ID ABU15172 standard; cDNA; 9263 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 39998.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 4.3%; Score 33; DB 4; Length 9263;
 Best Local Similarity 47.0%; Pred. No. 1e+02;
 RESULT 728
 ID AAS29831 standard; DNA; 32205 BP.
 DE Human cytoskeletal element-related polypeptide encoding genomic DNA #18.
 PN WO200155168-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 4.3%; Score 33; DB 4; Length 32205;
 Best Local Similarity 51.0%; Pred. No. 1.9e+02;
 RESULT 729
 ID AAS33426 standard; DNA; 32205 BP.
 DE DNA encoding human secreted protein, Seq ID No 709.
 PN WO200155326-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 4.3%; Score 33; DB 4; Length 32205;
 Best Local Similarity 51.0%; Pred. No. 1.9e+02;
 RESULT 730
 ID AAK85853 standard; DNA; 39969 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40665.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 4.3%; Score 33; DB 4; Length 39969;
 Best Local Similarity 51.0%; Pred. No. 2.1e+02;
 RESULT 731
 ID ADL15091 standard; DNA; 125729 BP.
 DE Human PHXBP1 pseudogene DNA for cancer treatment.
 PN WO2003068268-A2.
 PD 21-AUG-2003.
 PA (BIOI-) BIOINVENT INT AB.
 Query Match 4.3%; Score 33; DB 10; Length 125729;
 Best Local Similarity 51.7%; Pred. No. 3.5e+02;
 RESULT 732
 ID ADD50651 standard; DNA; 142299 BP.
 DE BAC sequence #2 containing hCMT DNA.
 PN US2003114399-A1.
 PD 19-JUN-2003.
 PA (BLAK/) BLAKELY R D.
 PA (APPA/) APPARUNDARAM S.
 PA (FERG/) FERGUSON S.
 Query Match 4.3%; Score 33; DB 10; Length 142299;
 Best Local Similarity 43.3%; Pred. No. 3.7e+02;
 RESULT 733
 ID AAK74680 standard; DNA; 8981 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:29492.
 PN WO200157182-A2.
 PD 09-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.3%; Score 32.8; DB 4; Length 8981;
Best Local Similarity 44.5%; Pred. No. 1.2e+02;
RESULT 734
ID AAQ10613 standard; DNA; 15672 BP.
DE Rianodin receptor gene.
PN JP03011098-A.
PD 18-JAN-1991.
PA (MITU) MITSUBISHI KASEI CORP.
Query Match 4.3%; Score 32.8; DB 2; Length 15672;
Best Local Similarity 58.0%; Pred. No. 1.5e+02;
RESULT 735
ID AAK96119 standard; DNA; 401 BP.
DE Human neuregulin gene single nucleotide polymorphism SNPSNRG997541.
PN WO200164876-A2.
PD 07-SEP-2001.
PA (DECO-) DECODE GENETICS EHF.
Query Match 4.3%; Score 32.6; DB 4; Length 401;
Best Local Similarity 63.3%; Pred. No. 32;
RESULT 736
ID AAK97612 standard; DNA; 401 BP.
DE Human neuregulin gene single nucleotide polymorphism SNPSNRG997541.
PN WO200164877-A2.
PD 07-SEP-2001.
PA (DECO-) DECODE GENETICS EHF.
Query Match 4.3%; Score 32.6; DB 4; Length 401;
Best Local Similarity 63.3%; Pred. No. 32;
RESULT 737
ID ABR00889 standard; DNA; 401 BP.
DE Human neuregulin-1-associated gene 1 fragment SEQ ID NO: 918.
PN US2002045577-A1.
PD 18-APR-2002.
PA (DECO-) DECODE GENETICS EHF.
Query Match 4.3%; Score 32.6; DB 6; Length 401;
Best Local Similarity 63.3%; Pred. No. 32;
RESULT 738
ID ABR02382 standard; DNA; 401 BP.
DE Human neuregulin-1-associated gene 1 fragment SEQ ID NO: 918.
PN US2002094954-A1.
PD 18-JUL-2002.
PA (DECO-) DECODE GENETICS EHF.
Query Match 4.3%; Score 32.6; DB 6; Length 401;
Best Local Similarity 63.3%; Pred. No. 32;
RESULT 739
ID ABZ16774 standard; DNA; 2000 BP.
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 4579.
PN WO200218655-A2.
PD 28-FEB-2002.
PA (SCRI) SCRIPPS RES INST.
Query Match 4.3%; Score 32.6; DB 6; Length 2000;
Best Local Similarity 49.7%; Pred. No. 67;
RESULT 740
ID ABN79830 standard; DNA; 2595 BP.
DE Fungal ZBC gene sequence #67.
PN WO200224865-A2.
PD 28-MAR-2002.
PA (MICR-) MICROBIA INC.
Query Match 4.3%; Score 32.6; DB 6; Length 2595;
Best Local Similarity 58.9%; Pred. No. 76;
RESULT 741
ID ABN79831 standard; DNA; 2595 BP.
DE Fungal ZBC gene sequence #68.
PN WO200224865-A2.
PD 28-MAR-2002.
PA (MICR-) MICROBIA INC.
Query Match 4.3%; Score 32.6; DB 6; Length 2595;
Best Local Similarity 58.9%; Pred. No. 76;
RESULT 742
ID AAS95264 standard; DNA; 2897 BP.
DE Long terminal repeat (LTR) retrotransposon #15.
PN WO200181598-A2.
PD 01-NOV-2001.

PA (JANC) JANSSEN PHARM NV.
Query Match 4.3%; Score 32.6; DB 6; Length 2897;
Best Local Similarity 48.2%; Pred. No. 80;
RESULT 743
ID AB112604 standard; cDNA; 4718 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 32294.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.3%; Score 32.6; DB 4; Length 4718;
Best Local Similarity 52.6%; Pred. No. 1e+02;
RESULT 744
Query Match 4.3%; Score 32.6; DB 4; Length 110000;
Best Local Similarity 63.3%; Pred. No. 4.4e+02;
RESULT 745
Query Match 4.3%; Score 32.6; DB 4; Length 110000;
Best Local Similarity 63.3%; Pred. No. 4.4e+02;
RESULT 746
Query Match 4.3%; Score 32.6; DB 5; Length 110000;
Best Local Similarity 49.1%; Pred. No. 4.4e+02;
RESULT 747
Query Match 4.3%; Score 32.6; DB 6; Length 110000;
Best Local Similarity 63.3%; Pred. No. 4.4e+02;
RESULT 748
Query Match 4.3%; Score 32.6; DB 6; Length 110000;
Best Local Similarity 63.3%; Pred. No. 4.4e+02;
RESULT 749
Query Match 4.3%; Score 32.6; DB 12; Length 110000;
Best Local Similarity 63.3%; Pred. No. 4.4e+02;
RESULT 750
ID ABV12272 standard; cDNA; 415 BP.
DE Human prostate expression marker cDNA 12263.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.2%; Score 32.4; DB 5; Length 415;
Best Local Similarity 54.1%; Pred. No. 37;
RESULT 751
ID ABV42340 standard; cDNA; 459 BP.
DE Human prostate expression marker cDNA 42331.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.2%; Score 32.4; DB 5; Length 459;
Best Local Similarity 54.1%; Pred. No. 39;
RESULT 752
ID ABV33417 standard; cDNA; 459 BP.
DE Human prostate expression marker cDNA 33408.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.2%; Score 32.4; DB 5; Length 459;
Best Local Similarity 54.1%; Pred. No. 39;
RESULT 753
ID ABV50091 standard; cDNA; 587 BP.
DE Human prostate expression marker cDNA 50082.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.2%; Score 32.4; DB 5; Length 587;
Best Local Similarity 49.4%; Pred. No. 44;
RESULT 754
ID ADR01578 standard; DNA; 746 BP.
DE A. gossvpii genomic DNA PAG1232RP.
PN US6239264-B1.
PD 29-MAY-2001.
PA (SYNG) SYNGENTA PARTICIPATIONS AG.
Query Match 4.2%; Score 32.4; DB 2; Length 746;
Best Local Similarity 56.4%; Pred. No. 49;
RESULT 755
ID AAZ29420 standard; cDNA; 804 BP.
DE Chenopodium rubrum CDK11 encoding cDNA.
PN WO9964599-A1.

PD 16-DEC-1999.
PA (MIAC) AGRIC & AGRI-FOOD CANADA.
PA (UYSA-) UNIV SASKATCHEWAN TECHNOLOGIES INC.
PA (CAN) NAT RES COUNCIL CANADA.
Query Match 4.2%; Score 32.4; DB 3; Length 804;
Best Local Similarity 46.8%; Pred. No. 51;
RESULT 756
ID AAD40768 standard; cDNA; 804 BP.
DE Chenopodium rubrum ICDK cDNA.
PD 27-JUN-2002.
PA (MIAC) CANADA MIN AGRIC & AGRI-FOOD CANADA.
PA (UYSA-) UNIV SASKATCHEWAN TECHNOLOGIES INC.
Query Match 4.2%; Score 32.4; DB 6; Length 804;
Best Local Similarity 46.8%; Pred. No. 51;
RESULT 757
ID ABL32274 standard; DNA; 6247 BP.
DE Human immune system associated gene SEQ ID NO: 247.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.2%; Score 32.4; DB 6; Length 6247;
Best Local Similarity 47.9%; Pred. No. 1.3e+02;
RESULT 758
ID ABK28222 standard; DNA; 11394 BP.
DE DNA transcription associated complementary genomic DNA #48.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.2%; Score 32.4; DB 6; Length 11394;
Best Local Similarity 51.4%; Pred. No. 1.8e+02;
RESULT 759
Query Match 4.2%; Score 32.4; DB 10; Length 110000;
Best Local Similarity 52.2%; Pred. No. 5e+02;
RESULT 760
Query Match 4.2%; Score 32.4; DB 10; Length 110000;
Best Local Similarity 56.6%; Pred. No. 5e+02;
RESULT 761
ID ACF65380 standard; DNA; 210710 BP.
DE Photorehabilitation luminescence nucleotide sequence #33.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 4.2%; Score 32.4; DB 10; Length 210710;
Best Local Similarity 56.6%; Pred. No. 6.8e+02;
RESULT 762
ID AAC01084 standard; cDNA; 414 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 1082.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 4.2%; Score 32.2; DB 3; Length 414;
Best Local Similarity 56.0%; Pred. No. 43;
RESULT 763
ID ABA63245 standard; DNA; 504 BP.
DE Human foetal liver single exon nucleic acid probe #11550.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 4.2%; Score 32.2; DB 4; Length 504;
Best Local Similarity 52.6%; Pred. No. 47;
RESULT 764
ID ABK53968 standard; cDNA; 537 BP.
DE Human head and neck tumour cDNA, SEQ ID NO 163.
PD 14-FEB-2002.
PA (CORI-) CORIXA CORP.
Query Match 4.2%; Score 32.2; DB 6; Length 537;
Best Local Similarity 50.3%; Pred. No. 48;
RESULT 765
ID AAC65137 standard; DNA; 855 BP.
DE Adipocyte complement related protein homologue zacrp2 degenerate DNA.

PD 26-OCT-2000.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 4.2%; Score 32.2; DB 3; Length 855;
Best Local Similarity 26.4%; Pred. No. 60;
RESULT 766
ID ADM66430 standard; DNA; 855 BP.
DE Degenerate DNA encoding human zacrp2.
PD 16-SEP-2003.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 4.2%; Score 32.2; DB 11; Length 855;
Best Local Similarity 26.4%; Pred. No. 60;
RESULT 767
ID ADL26865 standard; DNA; 855 BP.
DE Human zacrp2 degenerate DNA.
PD 05-FEB-2004.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 4.2%; Score 32.2; DB 12; Length 855;
Best Local Similarity 26.4%; Pred. No. 60;
RESULT 768
ID AAK69219 standard; DNA; 1390 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24031.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.2%; Score 32.2; DB 4; Length 1390;
Best Local Similarity 50.3%; Pred. No. 75;
RESULT 769
ID ABV25179 standard; cDNA; 1522 BP.
DE Human prostate expression marker cDNA 25170.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.2%; Score 32.2; DB 5; Length 1522;
Best Local Similarity 50.3%; Pred. No. 79;
RESULT 770
ID ABA16847 standard; DNA; 1860 BP.
DE Human nervous system related polynucleotide SEQ ID NO 9178.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.2%; Score 32.2; DB 5; Length 1860;
Best Local Similarity 47.3%; Pred. No. 86;
RESULT 771
ID ABA16846 standard; DNA; 1861 BP.
DE Human nervous system related polynucleotide SEQ ID NO 9177.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.2%; Score 32.2; DB 5; Length 1861;
Best Local Similarity 47.3%; Pred. No. 86;
RESULT 772
ID ADA53739 standard; cDNA; 2566 BP.
DE Human coding sequence, SEQ ID 1307.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 4.2%; Score 32.2; DB 10; Length 2566;
Best Local Similarity 47.3%; Pred. No. 1e+02;
RESULT 773
ID ADC30795 standard; cDNA; 2854 BP.
DE Human novel cDNA sequence, SEQ ID NO:877.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 4.2%; Score 32.2; DB 10; Length 2854;
Best Local Similarity 47.3%; Pred. No. 1.1e+02;
RESULT 774
ID ABL33642 standard; DNA; 6319 BP.
DE Human immune system associated gene SEQ ID NO: 1615.

PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.2%; Score 32.2; DB 6; Length 6319;
Best Local Similarity 52.5%; Pred. No. 1.5e+02;
RESULT 775
ID APT03059 standard; DNA; 8904 BP.
DE Human breast specific coding sequence SEQ ID NO: 64.
PN WO200240672-A2.
PD 23-MAY-2002.
PA (DIAD-) DIADEXUS INC.
Query Match 4.2%; Score 32.2; DB 6; Length 8904;
Best Local Similarity 54.7%; Pred. No. 1.8e+02;
RESULT 776
ID APT07637 standard; cDNA; 8905 BP.
DE Human breast cancer associated coding sequence SEQ ID NO: 116.
PN WO200264611-A1.
PD 22-AUG-2002.
PA (DIAD-) DIADEXUS INC.
Query Match 4.2%; Score 32.2; DB 6; Length 8905;
Best Local Similarity 54.7%; Pred. No. 1.8e+02;
RESULT 777
ID ADI72402 standard; DNA; 356 BP.
DE Human ovarian cancer DNA marker #5144.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.2%; Score 32; DB 5; Length 356;
Best Local Similarity 38.5%; Pred. No. 46;
RESULT 778
ID ADL37545 standard; DNA; 356 BP.
DE Human ovarian cancer DNA marker #11435.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.2%; Score 32; DB 5; Length 356;
Best Local Similarity 38.5%; Pred. No. 46;
RESULT 779
ID ACA46310 standard; DNA; 1026 BP.
DE Prokaryotic essential gene #27967.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.2%; Score 32; DB 8; Length 1026;
Best Local Similarity 50.7%; Pred. No. 75;
RESULT 780
ID AAS4908 standard; DNA; 1065 BP.
DE Staphylococcus aureus DNA for cellular proliferation protein #1220.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.2%; Score 32; DB 4; Length 1065;
Best Local Similarity 50.7%; Pred. No. 76;
RESULT 781
ID ACA52696 standard; DNA; 2130 BP.
DE Prokaryotic essential gene #34353.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.2%; Score 32; DB 8; Length 2130;
Best Local Similarity 47.9%; Pred. No. 1.1e+02;
RESULT 782
ID ADJ40496 standard; cDNA; 4536 BP.
DE Plant cDNA #1496.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.

PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RIQUE D.
PA (ZHUT/) ZHU T.
Query Match 4.2%; Score 32; DB 12; Length 4536;
Best Local Similarity 58.3%; Pred. No. 1.5e+02;
RESULT 783
ID AAO55753 standard; DNA; 4954 BP.
DE Escherichia coli genomic probe EC-34.
PN WO9401583-A1.
PD 20-JAN-1994.
PA (FUSO) FUSO PHARM IND LTD.
Query Match 4.2%; Score 32; DB 2; Length 4954;
Best Local Similarity 62.5%; Pred. No. 1.6e+02;
RESULT 784
ID ABZ77361 standard; DNA; 4954 BP.
DE Nucleotide sequence designated EC-34.
PN WO2002101037-A1.
PD 19-DEC-2002.
PA (FUSO) FUSO PHARM IND LTD.
Query Match 4.2%; Score 32; DB 8; Length 4954;
Best Local Similarity 62.5%; Pred. No. 1.6e+02;
RESULT 785
ID AAL51849 standard; DNA; 4954 BP.
DE Escherichia coli microbe identification-related DNA sequence #2.
PN WO200299133-A1.
PD 12-DEC-2002.
PA (FUSO) FUSO PHARM IND LTD.
Query Match 4.2%; Score 32; DB 10; Length 4954;
Best Local Similarity 62.5%; Pred. No. 1.6e+02;
RESULT 786
ID ABL32880 standard; DNA; 10197 BP.
DE Human immune system associated gene SEQ ID NO: 853.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.2%; Score 32; DB 6; Length 10197;
Best Local Similarity 47.9%; Pred. No. 2.2e+02;
RESULT 787
ID ABL92285 standard; DNA; 11015 BP.
DE Chemically treated DNA repair gene fragment complementary to #47.
PN WO200181622-A2.
PD 01-NOV-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.2%; Score 32; DB 6; Length 11015;
Best Local Similarity 51.4%; Pred. No. 2.3e+02;
RESULT 788
ID ABL49356 standard; DNA; 11015 BP.
DE Human polynucleotide associated with DNA replication SEQ ID NO 56.
PN WO200177377-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.2%; Score 32; DB 6; Length 11015;
Best Local Similarity 51.4%; Pred. No. 2.3e+02;
RESULT 789
ID AAD22336 standard; DNA; 11015 BP.
DE Chemically treated human genomic DNA #26 associated with DNA adducts.
PN WO200177378-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.2%; Score 32; DB 6; Length 11015;
Best Local Similarity 51.4%; Pred. No. 2.3e+02;
RESULT 790
ID ABL21130 standard; DNA; 19385 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 14863.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.2%; Score 32; DB 4; Length 19385;
Best Local Similarity 62.5%; Pred. No. 3e+02;
RESULT 791
ID ABV02994 standard; cDNA; 431 BP.

DE Human prostate expression marker cDNA 2985.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 4.2%; Score 31.8; DB 5; Length 431;
 Best Local Similarity 52.8%; Pred. No. 58;
 RESULT 792
 ID AAH06229 standard; cDNA; 693 BP.
 DE Human cDNA clone (5'-primer) SEQ ID NO:3064.
 PN EP1074617-A2.
 PD 07-FEB-2001.
 PA (HELI-) HELIX RES INST.
 Query Match 4.2%; Score 31.8; DB 4; Length 693;
 Best Local Similarity 56.1%; Pred. No. 72;
 RESULT 793
 ID AAK56975 standard; cDNA; 860 BP.
 DE Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:2035.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 4.2%; Score 31.8; DB 4; Length 860;
 Best Local Similarity 49.7%; Pred. No. 80;
 RESULT 794
 ID ADL12361 standard; cDNA; 894 BP.
 DE Human steroid-induced C3A liver cell cDNA #90.
 PN US6673549-B1.
 PD 06-JAN-2004.
 PA (INCY-) INCYTE CORP.
 Query Match 4.2%; Score 31.8; DB 12; Length 894;
 Best Local Similarity 48.1%; Pred. No. 81;
 RESULT 795
 ID ADI41892 standard; DNA; 1316 BP.
 DE Plant transcription factor polynucleotide #178.
 PN US2004019927-A1.
 PD 29-JAN-2004.
 PA (SHER/) SHERMAN B K.
 PA (RIEC/) RIECHMANN J L.
 PA (JIAN/) JIANG C.
 PA (HEAR/) HEARD J E.
 PA (HAAK/) HAAKE V.
 PA (CREE/) CREELMAN R A.
 PA (RATC/) RATCLIFFE O.
 PA (ADAM/) ADAM L J.
 PA (REUB/) REUBER T L.
 PA (KEDD/) KEDDIE J.
 PA (BROU/) BROUN P E.
 PA (PILG/) PILGRIM M L.
 PA (DUBE/) DUBELL A N.
 PA (PINE/) PINEDA O.
 PA (YUGG/) YU G.
 Query Match 4.2%; Score 31.8; DB 12; Length 1316;
 Best Local Similarity 50.3%; Pred. No. 97;
 RESULT 796
 ID ADO61836 standard; DNA; 1316 BP.
 DE Transcription factor G1863 coding sequence, SEQ ID 303.
 PN WO2004031349-A2.
 PD 15-APR-2004.
 PA (MEND-) MENDEL BIOTECHNOLOGY INC.
 Query Match 4.2%; Score 31.8; DB 12; Length 1316;
 Best Local Similarity 50.3%; Pred. No. 97;
 RESULT 797
 ID ADO63008 standard; DNA; 1316 BP.
 DE Transcription factor G1863 coding sequence, SEQ ID 1475.
 PN WO2004031349-A2.
 PD 15-APR-2004.
 PA (MEND-) MENDEL BIOTECHNOLOGY INC.
 Query Match 4.2%; Score 31.8; DB 12; Length 1316;
 Best Local Similarity 50.3%; Pred. No. 97;
 RESULT 798
 ID ADE37134 standard; cDNA; 1322 BP.
 DE Plant yield related polynucleotide clone G1863.
 PN WO2003014327-A2.
 PD 20-FEB-2003.

PA (MEND-) MENDEL BIOTECHNOLOGY INC.
 Query Match 4.2%; Score 31.8; DB 10; Length 1322;
 Best Local Similarity 50.3%; Pred. No. 97;
 RESULT 799
 ID AA293098 standard; DNA; 1438 BP.
 DE Thiosulphate sulphurtransferase gene of wheat.
 PN WO200006756-A1.
 PD 10-FEB-2000.
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 Query Match 4.2%; Score 31.8; DB 3; Length 1438;
 Best Local Similarity 57.6%; Pred. No. 1e+02;
 RESULT 800
 ID AAL60317 standard; cDNA; 4562 BP.
 DE Human polynucleotide SEQ ID NO 4306.
 PN WO200153312-A1.
 PD 26-JUL-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 4.2%; Score 31.8; DB 4; Length 4562;
 Best Local Similarity 56.1%; Pred. No. 1.7e+02;
 RESULT 801
 ID ABA18924 standard; DNA; 6554 BP.
 DE Human nervous system related polynucleotide SEQ ID NO 11255.
 PN WO200159063-A2.
 PD 16-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 4.2%; Score 31.8; DB 5; Length 6554;
 Best Local Similarity 49.1%; Pred. No. 2.1e+02;
 RESULT 802
 ID ABA18544 standard; DNA; 6554 BP.
 DE Human nervous system related polynucleotide SEQ ID NO 10875.
 PN WO200159063-A2.
 PD 16-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 4.2%; Score 31.8; DB 5; Length 6554;
 Best Local Similarity 49.1%; Pred. No. 2.1e+02;
 RESULT 803
 ID ABA18923 standard; DNA; 6567 BP.
 DE Human nervous system related polynucleotide SEQ ID NO 11254.
 PN WO200159063-A2.
 PD 16-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 4.2%; Score 31.8; DB 5; Length 6567;
 Best Local Similarity 49.1%; Pred. No. 2.1e+02;
 RESULT 804
 ID ABK31228 standard; DNA; 7234 BP.
 DE Signal transduction associated gene modified DNA #36.
 PN WO200200926-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 4.2%; Score 31.8; DB 6; Length 7234;
 Best Local Similarity 48.6%; Pred. No. 2.2e+02;
 RESULT 805
 ID ABK40017 standard; DNA; 18133 BP.
 DE Human chemically pretreated gene sequence #50 strand 1.
 PN WO200202806-A2.
 PD 10-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 4.2%; Score 31.8; DB 6; Length 18133;
 Best Local Similarity 49.1%; Pred. No. 3.3e+02;
 RESULT 806
 ID ABL32940 standard; DNA; 18133 BP.
 DE Human immune system associated gene SEQ ID NO: 913.
 PN WO200200928-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 4.2%; Score 31.8; DB 6; Length 18133;
 Best Local Similarity 49.1%; Pred. No. 3.3e+02;
 RESULT 807
 ID ABA19669 standard; DNA; 32247 BP.
 DE Human nervous system related polynucleotide SEQ ID NO 12000.
 PN WO200159063-A2.
 PD 16-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 4.2%; Score 31.8; DB 5; Length 32247;
Best Local Similarity 51.0%; Pred. No. 4.3e+02;
RESULT 808
Query Match 4.2%; Score 31.8; DB 6; Length 110000;
Best Local Similarity 46.6%; Pred. No. 7.6e+02;
RESULT 809
ID ADO79173 standard; DNA; 447894 BP.
DE KLF12 gene and surrounding region, SEQ ID 1.
Query Match 4.2%; Score 31.8; DB 12; Length 110000;
Best Local Similarity 48.1%; Pred. No. 7.6e+02;
RESULT 810
ID ABQ88207 standard; cDNA; 172570 BP.
DE Human osteoblast differentiation related cDNA SEQ ID NO 114.
PN WO200250301-A2.
PD 27-JUN-2002.
PA (GENE-) GENE LOGIC INC.
PA (PROC) PROCTER & GAMBLE CO.
Query Match 4.2%; Score 31.8; DB 6; Length 172570;
Best Local Similarity 56.1%; Pred. No. 9.4e+02;
RESULT 811
ID ADG99379 standard; DNA; 145 BP.
DE Kidney disease-associated gene-related mouse DNA sequence SeqID509.
PN WO2003091427-A1.
PD 06-NOV-2003.
PA (KANS-) KANSAI TECHNOLOGY LICENSING ORG CO LTD.
Query Match 4.1%; Score 31.6; DB 12; Length 145;
Best Local Similarity 56.9%; Pred. No. 40;
RESULT 812
ID AAK74840 standard; DNA; 424 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:29652.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.1%; Score 31.6; DB 4; Length 424;
Best Local Similarity 52.2%; Pred. No. 66;
RESULT 813
ID AAK74841 standard; DNA; 424 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:29653.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.1%; Score 31.6; DB 4; Length 424;
Best Local Similarity 52.2%; Pred. No. 66;
RESULT 814
ID ABZ54280 standard; cDNA; 541 BP.
DE Aspergillus oryzae polynucleotide SEQ ID NO 3393.
PN WO200279476-A1.
PD 10-OCT-2002.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (NARE-) NAT RES INST BREWING.
PA (NORO) NAT FOOD RES INST MIN AGRIC.
Query Match 4.1%; Score 31.6; DB 8; Length 541;
Best Local Similarity 60.5%; Pred. No. 74;
RESULT 815
ID AAX04323 standard; DNA; 632 BP.
DE Human secreted protein gene 13 clone HSAB142.
PN WO9856804-A1.
PD 17-DEC-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.1%; Score 31.6; DB 2; Length 632;
Best Local Similarity 55.5%; Pred. No. 79;
RESULT 816
ID ADA15611 standard; DNA; 1500 BP.
DE A. thaliana recombinant polynucleotide, SEQ ID NO:166.
PN US2003061637-A1.
PD 27-MAR-2003.
PA (JIAN/) JIANG C.
PA (BROU/) BROUN P.
PA (RIEC/) RIECHMANN J L.
PA (PINE/) PINEDA O.
PA (ZHAN/) ZHANG J.
PA (YUGG/) YU G.
PA (PILG/) PILGRIM M.

PA (KEDD/) KEDDIE J.
PA (HEAR/) HEARD J.
PA (REUB/) REUBER L.
PA (RATC/) RATCLIFFE O.
PA (ADAM/) ADAM L.
PA (SAMA/) SAMAHA R.
Query Match 4.1%; Score 31.6; DB 9; Length 1500;
Best Local Similarity 48.9%; Pred. No. 1.2e+02;
RESULT 817
ID ABL21672 standard; DNA; 2216 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 16489.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.1%; Score 31.6; DB 4; Length 2216;
Best Local Similarity 58.5%; Pred. No. 1.4e+02;
RESULT 818
ID ADO22935 standard; DNA; 2288 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5755.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 4.1%; Score 31.6; DB 12; Length 2288;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
RESULT 819
ID ABL31335 standard; DNA; 5252 BP.
DE Human immune system associated gene SEQ ID NO: 1108.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 31.6; DB 6; Length 5252;
Best Local Similarity 51.4%; Pred. No. 2.1e+02;
RESULT 820
ID ABK31398 standard; DNA; 5468 BP.
DE Signal transduction associated gene modified DNA #121.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 31.6; DB 6; Length 5468;
Best Local Similarity 51.4%; Pred. No. 2.2e+02;
RESULT 821
ID ABL70363 standard; DNA; 5468 BP.
DE Chemically treated cell signalling DNA sequence#127.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 31.6; DB 6; Length 5468;
Best Local Similarity 51.4%; Pred. No. 2.2e+02;
RESULT 822
ID AAS46583 standard; DNA; 6167 BP.
DE Tumour suppressor gene derived chemically modified sequence #305.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 31.6; DB 4; Length 6167;
Best Local Similarity 50.0%; Pred. No. 2.3e+02;
RESULT 823
ID ABL33838 standard; DNA; 6167 BP.
DE Human immune system associated gene SEQ ID NO: 1811.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 31.6; DB 6; Length 6167;
Best Local Similarity 50.0%; Pred. No. 2.3e+02;
RESULT 824
ID ABK31376 standard; DNA; 7037 BP.
DE Signal transduction associated gene modified DNA #110.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 31.6; DB 6; Length 7037;
Best Local Similarity 47.9%; Pred. No. 2.4e+02;
RESULT 825

ID AAD50032 standard; DNA; 9528 BP.
DE Human novel CpG-associated gene 1 (NCAG1) brain-expressed gene #1.
PN WO2002101044-A2.
PD 19-DEC-2002.
PA (JANC) JANSSEN PHARM NV.
Query Match 4.1%; Score 31.6; DB 10; Length 9528;
Best Local Similarity 46.1%; Pred. No. 2.8e+02;
RESULT 826
ID ABL34206 standard; DNA; 12601 BP.
DE Human immune system associated gene SEQ ID NO: 2179.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 31.6; DB 6; Length 12601;
Best Local Similarity 49.5%; Pred. No. 3.2e+02;
RESULT 827
ID ABL32673 standard; DNA; 16287 BP.
DE Human immune system associated gene SEQ ID NO: 646.
PN WO20020928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 31.6; DB 6; Length 16287;
Best Local Similarity 51.4%; Pred. No. 3.6e+02;
RESULT 828
ID AAD02701 standard; DNA; 27150 BP.
DE Human glycosyl sulfotransferase-6 (GST-6) genomic DNA #1.
PN WO200106015-A1.
PD 25-JAN-2001.
PA (REGC) UNIV CALIFORNIA.
Query Match 4.1%; Score 31.6; DB 4; Length 27150;
Best Local Similarity 46.1%; Pred. No. 4.6e+02;
RESULT 829
ID ABL10478 standard; cDNA; 29046 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 25916.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PERE) PE CORP NY.
Query Match 4.1%; Score 31.6; DB 4; Length 29046;
Best Local Similarity 50.0%; Pred. No. 4.8e+02;
RESULT 830
Query Match 4.1%; Score 31.6; DB 10; Length 110000;
Best Local Similarity 47.1%; Pred. No. 8.8e+02;
RESULT 831
ID ACH36149 standard; cDNA; 375 BP.
DE Human endothelial cell cDNA #4282.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 4.1%; Score 31.4; DB 9; Length 375;
Best Local Similarity 71.3%; Pred. No. 71;
RESULT 832
ID ABL81191 standard; cDNA; 441 BP.
DE Human ovarian cancer related cDNA clone SEQ ID NO:4169.
PN WO200192581-A2.
PD 06-DEC-2001.
PA (CORI-) CORIXA CORP.
Query Match 4.1%; Score 31.4; DB 6; Length 441;
Best Local Similarity 50.3%; Pred. No. 77;
RESULT 833
ID AAF64742 standard; cDNA; 451 BP.
DE Novel human polynucleotide, SEQ ID NO: 498.
PN WO200102568-A2.
PD 11-JAN-2001.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 4.1%; Score 31.4; DB 5; Length 451;
Best Local Similarity 56.2%; Pred. No. 78;
RESULT 834
ID ABT41119 standard; DNA; 452 BP.

DE Toxicity modelling related rat gene SEQ ID No 821.
PN WO200295000-A2.
PD 28-NOV-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 4.1%; Score 31.4; DB 10; Length 452;
Best Local Similarity 54.9%; Pred. No. 78;
RESULT 835
ID ADP72083 standard; DNA; 452 BP.
DE Renal toxin progression gene marker #672.
PN WO2004048598-A2.
PD 10-JUN-2004.
PA (GENE-) GENE LOGIC INC.
Query Match 4.1%; Score 31.4; DB 12; Length 452;
Best Local Similarity 54.9%; Pred. No. 78;
RESULT 836
ID ADD46193 standard; DNA; 603 BP.
DE Human gene BG203058, SEQ ID NO 11868.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 4.1%; Score 31.4; DB 10; Length 603;
Best Local Similarity 47.7%; Pred. No. 89;
RESULT 837
ID AAT67376 standard; DNA; 864 BP.
DE H. pylori cell envelope transporter protein ORF 13726562.aa.
PN WO9640893-A1.
PD 19-DEC-1996.
PA (ASTR) ASTRA AB.
Query Match 4.1%; Score 31.4; DB 2; Length 864;
Best Local Similarity 51.8%; Pred. No. 1.1e+02;
RESULT 838
ID AAT67872 standard; DNA; 1131 BP.
DE H. pylori transporter protein ORF 02ae1161lorf11.
PN WO9640893-A1.
PD 19-DEC-1996.
PA (ASTR) ASTRA AB.
Query Match 4.1%; Score 31.4; DB 2; Length 1131;
Best Local Similarity 51.8%; Pred. No. 1.2e+02;
RESULT 839
ID AAC79710 standard; cDNA; 1274 BP.
DE Human secreted protein gene 30 SEQ ID NO:40.
PN WO200058339-A2.
PD 05-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.1%; Score 31.4; DB 3; Length 1274;
Best Local Similarity 50.3%; Pred. No. 1.3e+02;
RESULT 840
ID AAV59612 standard; DNA; 1313 BP.
DE Human secreted protein gene 102 clone HE2BG03.
PN WO9839448-A2.
PD 11-SEP-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.1%; Score 31.4; DB 2; Length 1313;
Best Local Similarity 47.3%; Pred. No. 1.3e+02;
RESULT 841
ID ABS73599 standard; cDNA; 1313 BP.
DE Human cDNA #1 for novel secreted protein gene 102.
PN US6420526-B1.
PD 16-JUL-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.1%; Score 31.4; DB 6; Length 1313;
Best Local Similarity 47.3%; Pred. No. 1.3e+02;
RESULT 842
ID ACD82742 standard; cDNA; 1313 BP.
DE cDNA sequence #102 containing coding region of a human secreted protein.
PN US2003049618-A1.
PD 13-MAR-2003.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (SOPR/) SOPPET D R.
PA (CART/) CARTER K C.
PA (BEDN/) BEDNARIK D P.

PA (ENDR/) ENDRESS G A.
 PA (YUGG/) YU G.
 PA (NIJJ/) NI J.
 PA (FENG/) FENG P.
 PA (YOUN/) YOUNG P E.
 PA (GREE/) GREENE J M.
 PA (FERR/) FERRIE A M.
 PA (DUAN/) DUAN D R.
 PA (HUJJ/) HU J.
 PA (FLOR/) FLORENCE K A.
 PA (OLSE/) OLSEN H S.
 PA (FISC/) FISCHER C L.
 PA (EBNE/) EBNER R.
 PA (BREW/) BREWER L A.
 PA (MOOR/) MOORE P A.
 PA (SHIY/) SHI Y.
 PA (LAFLE/) LAFLEUR D W.
 PA (LIYY/) LI Y.
 PA (ZENG/) ZENG Z.
 PA (KYAW/) KYAW H.
 Query Match
 Best Local Similarity 4.1%; Score 31.4; DB 9; Length 1313;
 47.3%; Pred. No. 1.3e+02;
 RESULT 843
 ID ADI22827 standard; cDNA; 1313 BP.
 DE cDNA encoding novel human secreted protein seq id 112.
 PN US2003175858-A1.
 PD 18-SEP-2003.
 PA (RUBE/) RUBEN S M.
 PA (ROSE/) ROSEN C A.
 PA (SOPP/) SOPPET D R.
 PA (CART/) CARTER K C.
 PA (BEDN/) BEDNARIK D P.
 PA (ENDR/) ENDRESS G A.
 PA (YUGG/) YU G.
 PA (NIJJ/) NI J.
 PA (FENG/) FENG P.
 PA (YOUN/) YOUNG P E.
 PA (GREE/) GREENE J M.
 PA (FERR/) FERRIE A M.
 PA (DUAN/) DUAN D R.
 PA (HUJJ/) HU J.
 PA (FLOR/) FLORENCE K A.
 PA (OLSE/) OLSEN H S.
 PA (FISC/) FISCHER C L.
 PA (EBNE/) EBNER R.
 PA (BREW/) BREWER L A.
 PA (MOOR/) MOORE P A.
 PA (SHIY/) SHI Y.
 PA (LAFLE/) LAFLEUR D W.
 PA (LIYY/) LI Y.
 PA (ZENG/) ZENG Z.
 PA (KYAW/) KYAW H.
 Query Match
 Best Local Similarity 4.1%; Score 31.4; DB 10; Length 1313;
 47.3%; Pred. No. 1.3e+02;
 RESULT 844
 ID ADH73829 standard; cDNA; 1313 BP.
 DE Human secreted protein cDNA #102.
 PN US2003225248-A1.
 PD 04-DEC-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match
 Best Local Similarity 4.1%; Score 31.4; DB 12; Length 1313;
 47.3%; Pred. No. 1.3e+02;
 RESULT 845
 ID AAF32735 standard; cDNA; 1893 BP.
 DE Human secreted protein gene 37 SEQ ID NO:47.
 PN WO20007255-A1.
 PD 21-DEC-2000.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match
 Best Local Similarity 4.1%; Score 31.4; DB 4; Length 1893;
 56.2%; Pred. No. 1.5e+02;
 RESULT 846
 ID ACA7527 standard; DNA; 1896 BP.
 DE Prokaryotic essential gene #29184.

PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match
 Best Local Similarity 4.1%; Score 31.4; DB 8; Length 1896;
 48.1%; Pred. No. 1.5e+02;
 RESULT 847
 ID AAV59644 standard; DNA; 1944 BP.
 DE Human secreted protein gene 134 clone HPMGD24.
 PN WO9839448-A2.
 PD 11-SEP-1998.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match
 Best Local Similarity 4.1%; Score 31.4; DB 2; Length 1944;
 71.9%; Pred. No. 1.5e+02;
 RESULT 848
 ID ABS73631 standard; cDNA; 1944 BP.
 DE Human cDNA #1 for novel secreted protein gene 134.
 PN US6420526-B1.
 PD 16-JUL-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match
 Best Local Similarity 4.1%; Score 31.4; DB 6; Length 1944;
 71.9%; Pred. No. 1.5e+02;
 RESULT 849
 ID ACD82774 standard; cDNA; 1944 BP.
 DE cDNA sequence #134 containing coding region of a human secreted protein.
 PN US2003049618-A1.
 PD 13-MAR-2003.
 PA (RUBE/) RUBEN S M.
 PA (ROSE/) ROSEN C A.
 PA (SOPP/) SOPPET D R.
 PA (CART/) CARTER K C.
 PA (BEDN/) BEDNARIK D P.
 PA (ENDR/) ENDRESS G A.
 PA (YUGG/) YU G.
 PA (NIJJ/) NI J.
 PA (FENG/) FENG P.
 PA (YOUN/) YOUNG P E.
 PA (GREE/) GREENE J M.
 PA (FERR/) FERRIE A M.
 PA (DUAN/) DUAN D R.
 PA (HUJJ/) HU J.
 PA (FLOR/) FLORENCE K A.
 PA (OLSE/) OLSEN H S.
 PA (FISC/) FISCHER C L.
 PA (EBNE/) EBNER R.
 PA (BREW/) BREWER L A.
 PA (MOOR/) MOORE P A.
 PA (SHIY/) SHI Y.
 PA (LAFLE/) LAFLEUR D W.
 PA (LIYY/) LI Y.
 PA (ZENG/) ZENG Z.
 PA (KYAW/) KYAW H.
 Query Match
 Best Local Similarity 4.1%; Score 31.4; DB 9; Length 1944;
 71.9%; Pred. No. 1.5e+02;
 RESULT 850
 ID ADI22859 standard; cDNA; 1944 BP.
 DE cDNA encoding novel human secreted protein seq id 144.
 PN US2003175858-A1.
 PD 18-SEP-2003.
 PA (RUBE/) RUBEN S M.
 PA (ROSE/) ROSEN C A.
 PA (SOPP/) SOPPET D R.
 PA (CART/) CARTER K C.
 PA (BEDN/) BEDNARIK D P.
 PA (ENDR/) ENDRESS G A.
 PA (YUGG/) YU G.
 PA (NIJJ/) NI J.
 PA (FENG/) FENG P.
 PA (YOUN/) YOUNG P E.
 PA (GREE/) GREENE J M.
 PA (FERR/) FERRIE A M.
 PA (DUAN/) DUAN D R.
 PA (HUJJ/) HU J.
 PA (FLOR/) FLORENCE K A.
 PA (OLSE/) OLSEN H S.
 PA (FISC/) FISCHER C L.
 PA (EBNE/) EBNER R.
 PA (BREW/) BREWER L A.
 PA (MOOR/) MOORE P A.
 PA (SHIY/) SHI Y.
 PA (LAFLE/) LAFLEUR D W.
 PA (LIYY/) LI Y.
 PA (ZENG/) ZENG Z.
 PA (KYAW/) KYAW H.
 Query Match
 Best Local Similarity 4.1%; Score 31.4; DB 9; Length 1944;
 71.9%; Pred. No. 1.5e+02;

PA (OLSE//) OLSEN H S.
PA (FISC//) FISCHER C L.
PA (EBNE//) EBNER R.
PA (BREW//) BREWER L A.
PA (MOOR//) MOORE P A.
PA (SHIY//) SHI Y.
PA (LAFLE//) LAFLEUR D W.
PA (LIYY//) LI Y.
PA (ZENGE//) ZENG Z.
PA (KYAW//) KYAW H.
Query Match
Best Local Similarity 4.1%; Score 31.4; DB 10; Length 1944;
RESULT 851
ID ADH73861 standard; cDNA; 1944 BP.
DE Human secreted protein cDNA #134.
PN US2003225248-A1.
PD 04-DEC-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 4.1%; Score 31.4; DB 12; Length 1944;
RESULT 852
ID AAC36715 standard; DNA; 1993 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 14818.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 4.1%; Score 31.4; DB 3; Length 1993;
RESULT 853
ID AAF26568 standard; DNA; 2108 BP.
DE DNA encoding human secreted protein #22.
PN WO200076531-A1.
PD 21-DEC-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 4.1%; Score 31.4; DB 4; Length 2108;
RESULT 854
ID AAF45111 standard; cDNA; 2266 BP.
DE Human secreted protein coding sequence SEQ ID NO: 50.
PN WO200077023-A1.
PD 21-DEC-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 4.1%; Score 31.4; DB 4; Length 2266;
RESULT 855
ID AAS23423 standard; DNA; 2307 BP.
DE Candida albicans essential gene CAYMR277W (FCP1).
PN WO200160975-A2.
PD 23-AUG-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 4.1%; Score 31.4; DB 4; Length 2307;
RESULT 856
ID ABZ31771 standard; DNA; 2307 BP.
DE Candida albicans essential gene SEQ ID NO 6058.
PN WO200253728-A2.
PD 11-JUL-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 4.1%; Score 31.4; DB 6; Length 2307;
RESULT 857
ID ABL25870 standard; DNA; 2333 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 29083.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 4.1%; Score 31.4; DB 4; Length 2333;
RESULT 858
ID AAH15891 standard; cDNA; 2349 BP.
DE Human cDNA sequence SEQ ID NO:14430.
PN EPI074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.

Query Match
Best Local Similarity 4.1%; Score 31.4; DB 4; Length 2349;
RESULT 859
ID AAH77802 standard; DNA; 2349 BP.
DE Nucleotide sequence of a human liver-associated gene.
PN WO200109318-A1.
PD 08-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match
Best Local Similarity 4.1%; Score 31.4; DB 4; Length 2349;
RESULT 860
ID ABL27076 standard; DNA; 2879 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 32701.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 4.1%; Score 31.4; DB 4; Length 2879;
RESULT 861
ID AAC75938 standard; cDNA; 4547 BP.
DE Human ORFX ORF1493 polynucleotide sequence SEQ ID NO:2985.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 4.1%; Score 31.4; DB 3; Length 4547;
RESULT 862
ID AAI58531 standard; cDNA; 4562 BP.
DE Human polynucleotide SEQ ID NO 734.
PN WO200153312-A1.
PD 28-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 4.1%; Score 31.4; DB 4; Length 4562;
RESULT 863
ID ADQ98748 standard; cDNA; 4562 BP.
DE DNA encoding human GPCR-like protein seqid 418.
PN US6569662-B1.
PD 27-MAY-2003.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 4.1%; Score 31.4; DB 5; Length 4562;
RESULT 864
ID ADB48508 standard; cDNA; 4562 BP.
DE Novel human cDNA SEQ ID NO 418.
PN US2003104529-A1.
PD 05-JUN-2003.
PA (ZHOU//) ZHOU P.
PA (TANG//) TANG Y T.
PA (LIUC//) LIU C.
PA (ASUN//) ASUNDI V.
PA (DRMA//) DRMANAC R T.
Query Match
Best Local Similarity 4.1%; Score 31.4; DB 9; Length 4562;
RESULT 865
ID AAK52963 standard; cDNA; 4563 BP.
DE Human polynucleotide SEQ ID NO 2492.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 4.1%; Score 31.4; DB 4; Length 4563;
RESULT 866
ID ADQ20329 standard; DNA; 4563 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 3149.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match
Best Local Similarity 4.1%; Score 31.4; DB 12; Length 4563;
RESULT 867
ID AAK51979 standard; cDNA; 4567 BP.
DE Human polynucleotide SEQ ID NO 524.

PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.1%; Score 31.4; DB 4; Length 4567;
Best Local Similarity 56.2%; Pred. No. 2.3e+02;
RESULT 868
ID AAB24065 standard; DNA; 4590 BP.
DE Yeast AOD9604-associated DNA sequence, SEQ ID NO:1.
PN WO200133977-A1.
PD 17-MAY-2001.
PA (META-) METABOLIC PHARM LTD.
Query Match 4.1%; Score 31.4; DB 5; Length 4590;
Best Local Similarity 14.8%; Pred. No. 2.3e+02;
RESULT 869
ID ADL61925 standard; DNA; 4689 BP.
DE Human ovarian cancer DNA marker #20137.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.1%; Score 31.4; DB 5; Length 4689;
Best Local Similarity 56.2%; Pred. No. 2.3e+02;
RESULT 870
ID ADQ24340 standard; DNA; 4696 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7160.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 4.1%; Score 31.4; DB 12; Length 4696;
Best Local Similarity 56.2%; Pred. No. 2.3e+02;
RESULT 871
ID ABQ76258 standard; DNA; 4699 BP.
DE Human 7B6 DNA.
PN WO200264777-A2.
PD 22-AUG-2002.
PA (BADI-) BASF-LYNX BIOSCIENCE AG.
Query Match 4.1%; Score 31.4; DB 6; Length 4699;
Best Local Similarity 56.2%; Pred. No. 2.3e+02;
RESULT 872
ID ABL33916 standard; DNA; 5464 BP.
DE Human immune system associated gene SEQ ID NO: 1889.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 31.4; DB 6; Length 5464;
Best Local Similarity 54.9%; Pred. No. 2.5e+02;
RESULT 873
ID ABK31452 standard; DNA; 5464 BP.
DE Signal transduction associated gene modified DNA #148.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 31.4; DB 6; Length 5464;
Best Local Similarity 54.9%; Pred. No. 2.5e+02;
RESULT 874
ID ABL70429 standard; DNA; 5464 BP.
DE Chemically treated cell signalling DNA sequence#160.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 31.4; DB 6; Length 5464;
Best Local Similarity 54.9%; Pred. No. 2.5e+02;
RESULT 875
ID AAS63340 standard; DNA; 6207 BP.
DE Chemically pretreated metabolism associated gene #35.
PN WO200176451-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 31.4; DB 6; Length 6207;
Best Local Similarity 51.8%; Pred. No. 2.7e+02;
RESULT 876
ID AAK89991 standard; DNA; 12244 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 3567.
PN WO200155314-A2.

PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.1%; Score 31.4; DB 4; Length 12244;
Best Local Similarity 64.4%; Pred. No. 3.6e+02;
RESULT 877
ID ABL70575 standard; DNA; 19576 BP.
DE Chemically treated cell signalling DNA sequence#233.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 31.4; DB 6; Length 19576;
Best Local Similarity 47.3%; Pred. No. 4.5e+02;
RESULT 878
ID AAS61258 standard; DNA; 19576 BP.
DE Human gene regulation-associated gene oligonucleotide #213.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 31.4; DB 6; Length 19576;
Best Local Similarity 47.3%; Pred. No. 4.5e+02;
RESULT 879
ID AAK77120 standard; DNA; 22977 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:31932.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.1%; Score 31.4; DB 4; Length 22977;
Best Local Similarity 57.7%; Pred. No. 4.9e+02;
RESULT 880
ID AAF27996 standard; DNA; 48000 BP.
DE Human calcium sensitive potassium channel beta3 subunits coding sequence.
PN WO200105828-A1.
PD 25-JAN-2001.
PA (MERI-) MERCK & CO INC.
Query Match 4.1%; Score 31.4; DB 4; Length 48000;
Best Local Similarity 46.5%; Pred. No. 6.9e+02;
RESULT 881
ID ABL33916 standard; DNA; 5464 BP.
DE Human immune system associated gene SEQ ID NO: 1889.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 31.4; DB 6; Length 5464;
Best Local Similarity 54.9%; Pred. No. 2.5e+02;
RESULT 882
ID ADQ19901 standard; DNA; 158811 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2720.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 4.1%; Score 31.4; DB 12; Length 158811;
Best Local Similarity 46.9%; Pred. No. 1.2e+03;
RESULT 883
ID ADC24763 standard; DNA; 334462 BP.
DE Human wild type HNL4X genomic sequence.
PN WO2003045998-A2.
PD 05-JUN-2003.
PA (INRM-) INSERM INST NAT SANTE & RECH MEDICALE.
PA (INSP-) INST PASTEUR.
PA (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.
Query Match 4.1%; Score 31.4; DB 10; Length 334462;
Best Local Similarity 64.4%; Pred. No. 1.6e+03;
RESULT 884
ID ABV49114 standard; cDNA; 319 BP.
DE Human prostate expression marker cDNA 49105.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.1%; Score 31.2; DB 5; Length 319;
Best Local Similarity 60.7%; Pred. No. 76;
RESULT 885
ID ABV19340 standard; cDNA; 387 BP.
DE Human prostate expression marker cDNA 19331.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.1%; Score 31.2; DB 5; Length 387;
Best Local Similarity 60.7%; Pred. No. 83;

RESULT 886
ID ACH48040 standard; cDNA; 452 BP.
DE Human lung tumour cDNA #173.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 4.1%; Score 31.2; DB 9; Length 452;
Best Local Similarity 58.7%; Pred. No. 90;
RESULT 887
ID ABV94430 standard; cDNA; 520 BP.
DE Breast carcinoma related nucleotide sequence SEQ ID NO:421.
PN WO200246467-A2.
PD 13-JUN-2002.
PA (IPSO-) IPSOGEN.
Query Match 4.1%; Score 31.2; DB 6; Length 520;
Best Local Similarity 58.7%; Pred. No. 96;
RESULT 888
ID ADF79804 standard; DNA; 532 BP.
DE Leukaemia-related DNA sequence #360.
PN WO2003039443-A2.
PD 15-MAY-2003.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA (YLU-) UNIV LUDWIG MAXIMILIANS.
PA (HAFE/) HAERLACH T.
PA (SCHO/) SCHOCH C.
PA (KERN/) KERN W.
Query Match 4.1%; Score 31.2; DB 10; Length 532;
Best Local Similarity 58.7%; Pred. No. 97;
RESULT 889
ID ABS73206 standard; DNA; 747 BP.
DE Human translocation (4; 11) (q21; q23) #1.
PN WO200269900-A2.
PD 12-SEP-2002.
PA (CONF-) CONFORMA THERAPEUTICS CORP.
Query Match 4.1%; Score 31.2; DB 6; Length 747;
Best Local Similarity 57.0%; Pred. No. 11e+02;
RESULT 890
ID AAA98305 standard; DNA; 982 BP.
DE Human MSH6 fragment 8/exon 8 to 10 DNA.
PN DE1909878-A1.
PD 07-SEP-2000.
PA (UYDR) UNIV DRESDEN TECH.
Query Match 4.1%; Score 31.2; DB 3; Length 982;
Best Local Similarity 66.2%; Pred. No. 1.3e+02;
RESULT 891
ID ACF72045 standard; DNA; 1146 BP.
DE Photorehabdus luminescens nucleotide sequence #10512.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 4.1%; Score 31.2; DB 10; Length 1146;
Best Local Similarity 50.7%; Pred. No. 1.4e+02;
RESULT 892
ID AAC50967 standard; DNA; 1232 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 66790.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.1%; Score 31.2; DB 3; Length 1232;
Best Local Similarity 49.1%; Pred. No. 1.4e+02;
RESULT 893
ID AAI68576 standard; DNA; 1355 BP.
DE L. esculentum SUT2 encoding DNA fragment.
PN WO200173086-A2.
PD 04-OCT-2001.
PA (FROM/) FROMMER W.
Query Match 4.1%; Score 31.2; DB 4; Length 1355;
Best Local Similarity 51.4%; Pred. No. 1.5e+02;
RESULT 894

ID ADA29148 standard; DNA; 1413 BP.
DE DNA encoding Acinetobacter baumannii protein #435.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.1%; Score 31.2; DB 9; Length 1413;
Best Local Similarity 57.0%; Pred. No. 1.5e+02;
RESULT 895
ID AAH50960 standard; cDNA; 1466 BP.
DE Plastidial delta 9 ACP desaturase partial clone nucleotide sequence.
PN WO200138484-A2.
PD 31-MAY-2001.
PA (BADI) BASF PLANT SCI GMBH.
Query Match 4.1%; Score 31.2; DB 5; Length 1466;
Best Local Similarity 60.7%; Pred. No. 1.6e+02;
RESULT 896
ID AAC50961 standard; DNA; 1731 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 66767.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.1%; Score 31.2; DB 3; Length 1731;
Best Local Similarity 49.1%; Pred. No. 1.7e+02;
RESULT 897
ID AAC44647 standard; DNA; 1735 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 43597.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.1%; Score 31.2; DB 3; Length 1735;
Best Local Similarity 49.1%; Pred. No. 1.7e+02;
RESULT 898
ID AAI68593 standard; DNA; 1818 BP.
DE S. tuberosum SUT2 encoding DNA.
PN WO200173086-A2.
PD 04-OCT-2001.
PA (FROM/) FROMMER W.
Query Match 4.1%; Score 31.2; DB 4; Length 1818;
Best Local Similarity 51.4%; Pred. No. 1.7e+02;
RESULT 899
ID ACF79843 standard; cDNA; 2621 BP.
DE Mouse anion exchanger SLC26A11 cDNA.
PN WO2003072756-A2.
PD 04-SEP-2003.
PA (UYVA-) UNIV VANDERBILT.
PA (EGHM) BRIGHAM & WOMENS HOSPITAL INC.
PA (UYCA-) UNIV CASE WESTERN RESERVE.
Query Match 4.1%; Score 31.2; DB 10; Length 2621;
Best Local Similarity 55.6%; Pred. No. 2e+02;
RESULT 900
ID ADL83155 standard; cDNA; 3262 BP.
DE Human PRO84309 cDNA, SEQ ID 357.
PN WO2004024097-A2.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 31.2; DB 12; Length 3262;
Best Local Similarity 66.2%; Pred. No. 2.3e+02;
RESULT 901
ID ADO19324 standard; cDNA; 3262 BP.
DE Human PRO polynucleotide #128.
PN WO2004043361-A2.
PD 27-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 31.2; DB 12; Length 3262;
Best Local Similarity 66.2%; Pred. No. 2.3e+02;
RESULT 902
ID AAS73923 standard; cDNA; 3650 BP.
DE DNA encoding novel human diagnostic protein #9727.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSB-) HYSSEQ INC.
Query Match 4.1%; Score 31.2; DB 5; Length 3650;
Best Local Similarity 52.3%; Pred. No. 2.4e+02;
RESULT 903
ID AAL06092 standard; DNA; 4800 BP.

DE Human reproductive system related antigen DNA SEQ ID NO: 8780.
 PN WO200155320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 4.1%; Score 31.2; DB 4; Length 4800;
 Best Local Similarity 55.6%; Pred. No. 2.7e+02;
 RESULT 904
 ID ABL98657 standard; DNA; 4800 BP.
 DE Human testicular antigen encoding DNA fragment SEQ ID NO: 3309.
 PN WO200155317-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 4.1%; Score 31.2; DB 4; Length 4800;
 Best Local Similarity 55.6%; Pred. No. 2.7e+02;
 RESULT 905
 ID AAL06093 standard; DNA; 4845 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 8781.
 PN WO200155320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 4.1%; Score 31.2; DB 4; Length 4845;
 Best Local Similarity 55.6%; Pred. No. 2.7e+02;
 RESULT 906
 ID ABL98658 standard; DNA; 4845 BP.
 DE Human testicular antigen encoding DNA fragment SEQ ID NO: 3310.
 PN WO200155317-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 4.1%; Score 31.2; DB 4; Length 4845;
 Best Local Similarity 55.6%; Pred. No. 2.7e+02;
 RESULT 907
 ID ABK31540 standard; DNA; 6045 BP.
 DE Signal transduction associated gene modified DNA #192.
 PN WO200200926-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 4.1%; Score 31.2; DB 6; Length 6045;
 Best Local Similarity 49.4%; Pred. No. 3e+02;
 RESULT 908
 ID ABL70623 standard; DNA; 6045 BP.
 DE Chemically treated cell signalling DNA sequence#257.
 PN WO200202807-A2.
 PD 10-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 4.1%; Score 31.2; DB 6; Length 6045;
 Best Local Similarity 49.4%; Pred. No. 3e+02;
 RESULT 909
 ID RAZ23433 standard; DNA; 6450 BP.
 DE Human estrogen receptor DNA.
 PN WO9945944-A1.
 PD 16-SEP-1999.
 PA (BURN-) BURNHAM INST.
 Query Match 4.1%; Score 31.2; DB 2; Length 6450;
 Best Local Similarity 58.7%; Pred. No. 3.1e+02;
 RESULT 910
 ID ABK9695 standard; DNA; 6450 BP.
 DE Estrogen receptor alpha nucleic acid comprising A908G mutation, #1.
 PN WO200257283-A1.
 PD 25-JUL-2002.
 PA (BAYU) BAYLOR COLLEGE MEDICINE.
 Query Match 4.1%; Score 31.2; DB 6; Length 6450;
 Best Local Similarity 58.7%; Pred. No. 3.1e+02;
 RESULT 911
 ID ABK9703 standard; DNA; 6450 BP.
 DE Estrogen receptor alpha nucleic acid comprising A908G mutation, #7.
 PN WO200257283-A1.
 PD 25-JUL-2002.
 PA (BAYU) BAYLOR COLLEGE MEDICINE.
 Query Match 4.1%; Score 31.2; DB 6; Length 6450;
 Best Local Similarity 58.7%; Pred. No. 3.1e+02;
 RESULT 912
 ID ABV94431 standard; cDNA; 6450 BP.
 DE Breast carcinoma related nucleotide sequence SEQ ID NO:422.

PN WO200246467-A2.
 PD 13-JUN-2002.
 PA (IPSO-) IPSOGEN.
 Query Match 4.1%; Score 31.2; DB 6; Length 6450;
 Best Local Similarity 58.7%; Pred. No. 3.1e+02;
 RESULT 913
 ID AB223389 standard; cDNA; 6450 BP.
 DE Reverse complement of human oestrogen receptor alpha cDNA.
 PN WO200270699-A2.
 PD 12-SEP-2002.
 PA (LION-) LION BIOSCIENCE AG.
 Query Match 4.1%; Score 31.2; DB 6; Length 6450;
 Best Local Similarity 58.7%; Pred. No. 3.1e+02;
 RESULT 914
 ID AB223388 standard; cDNA; 6450 BP.
 DE Nucleotide sequence of human oestrogen receptor alpha.
 PN WO200270699-A2.
 PD 12-SEP-2002.
 PA (LION-) LION BIOSCIENCE AG.
 Query Match 4.1%; Score 31.2; DB 6; Length 6450;
 Best Local Similarity 58.7%; Pred. No. 3.1e+02;
 RESULT 915
 ID ABX12085 standard; cDNA; 6450 BP.
 DE cDNA encoding a human oestrogen receptor.
 PN US2002164581-A1.
 PD 07-NOV-2002.
 PA (CHAN/) CHANG C.
 Query Match 4.1%; Score 31.2; DB 8; Length 6450;
 Best Local Similarity 58.7%; Pred. No. 3.1e+02;
 RESULT 916
 ID ACC50140 standard; cDNA; 6450 BP.
 DE Breast cancer associated cDNA sequence SEQ ID NO:127.
 PN WO2003004989-A2.
 PD 16-JAN-2003.
 PA (MILL-) MILLENIUM PHARM INC.
 Query Match 4.1%; Score 31.2; DB 8; Length 6450;
 Best Local Similarity 58.7%; Pred. No. 3.1e+02;
 RESULT 917
 ID ABX93797 standard; cDNA; 6450 BP.
 DE Human oestrogen receptor alpha (ER-alpha) cDNA.
 PN US2002187495-A1.
 PD 12-DEC-2002.
 PA (HERR/) HERRINGTON D M.
 PA (HOWA/) HOWARD T D.
 PA (HAWK/) HAWKINS G A.
 PA (MEYE/) MEYERS D A.
 Query Match 4.1%; Score 31.2; DB 8; Length 6450;
 Best Local Similarity 58.7%; Pred. No. 3.1e+02;
 RESULT 918
 ID ADB81383 standard; DNA; 6450 BP.
 DE DNA sequence of the human oestrogen receptor alpha mRNA.
 PN WO2003052072-A2.
 PD 26-JUN-2003.
 PA (ISIS-) ISIS PHARM INC.
 Query Match 4.1%; Score 31.2; DB 10; Length 6450;
 Best Local Similarity 58.7%; Pred. No. 3.1e+02;
 RESULT 919
 ID ADD25499 standard; DNA; 6450 BP.
 DE Binding domain-immunoglobulin fusion protein-associated DNA #34.
 PN US2003118592-A1.
 PD 26-JUN-2003.
 PA (GENE-) GENE-CRAFT INC.
 Query Match 4.1%; Score 31.2; DB 10; Length 6450;
 Best Local Similarity 58.7%; Pred. No. 3.1e+02;
 RESULT 920
 ID ABE12135 standard; DNA; 6450 BP.
 DE Human oestrogen receptor alpha DNA.
 PN US2003199472-A1.
 PD 23-OCT-2003.
 PA (TEXA) UNIV TEXAS SYSTEM.
 PA (NOUN) UNIV NORTHWESTERN.
 Query Match 4.1%; Score 31.2; DB 10; Length 6450;
 Best Local Similarity 58.7%; Pred. No. 3.1e+02;

RESULT 921
 ID ADF76402 standard; cDNA; 6450 BP.
 DE Novel human secreted and transmembrane protein cDNA SeqID 75.
 PN WO2003072035-A2.
 PD 04-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.1%; Score 31.2; DB 10; Length 6450;
 Best Local Similarity 58.7%; Pred. No. 3.1e+02;
 RESULT 922
 ID ADG89355 standard; DNA; 6450 BP.
 DE Cancer detection method related gene #18.
 PN WO2003078662-A1.
 PD 23-SEP-2003.
 PA (GENO-) GENOMIC HEALTH INC.
 Query Match 4.1%; Score 31.2; DB 10; Length 6450;
 Best Local Similarity 58.7%; Pred. No. 3.1e+02;
 RESULT 923
 ID ADF83093 standard; DNA; 6450 BP.
 DE Human testicular orphan nuclear receptor 4 (TR4) DNA.
 PN WO2003100028-A2.
 PD 04-DEC-2003.
 PA (UVRP) UNIV ROCHESTER.
 Query Match 4.1%; Score 31.2; DB 12; Length 6450;
 Best Local Similarity 58.7%; Pred. No. 3.1e+02;
 RESULT 924
 ID ADF73229 standard; cDNA; 6450 BP.
 DE Human androgen receptor nucleotide sequence SEQ ID NO:25.
 PN WO2003103595-A2.
 PD 18-DEC-2003.
 PA (UVRP) UNIV ROCHESTER.
 Query Match 4.1%; Score 31.2; DB 12; Length 6450;
 Best Local Similarity 58.7%; Pred. No. 3.1e+02;
 RESULT 925
 ID ADP07306 standard; DNA; 6450 BP.
 DE Human ESR1 DNA.
 PN DE10255104-A1.
 PD 11-MAR-2004.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 4.1%; Score 31.2; DB 12; Length 6450;
 Best Local Similarity 58.7%; Pred. No. 3.1e+02;
 RESULT 926
 ID ADP03662 standard; DNA; 6450 BP.
 DE Human nuclear receptor protein gene SeqID36.
 PN WO2004045369-A2.
 PD 03-JUN-2004.
 PA (NURA-) NURA INC.
 Query Match 4.1%; Score 31.2; DB 12; Length 6450;
 Best Local Similarity 58.7%; Pred. No. 3.1e+02;
 RESULT 927
 ID ACC46160 standard; cDNA; 6468 BP.
 DE Human dithp receptor-encoding cDNA.
 PN WO200297031-A2.
 PD 05-DEC-2002.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 4.1%; Score 31.2; DB 8; Length 6468;
 Best Local Similarity 58.7%; Pred. No. 3.1e+02;
 RESULT 928
 ID ADB81390 standard; DNA; 8566 BP.
 DE Concatenated sequence of exons from chromosome 6 related to ESR-alpha.
 PN WO2003052072-A2.
 PD 26-JUN-2003.
 PA (ISIS-) ISIS PHARM INC.
 Query Match 4.1%; Score 31.2; DB 10; Length 8566;
 Best Local Similarity 58.7%; Pred. No. 3.5e+02;
 RESULT 929
 ID ABL14994 standard; cDNA; 13843 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 39464.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 4.1%; Score 31.2; DB 4; Length 13843;
 Best Local Similarity 52.3%; Pred. No. 4.4e+02;
 RESULT 930

ID AAL04663 standard; DNA; 22073 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 7351.
 PN WO200155320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 4.1%; Score 31.2; DB 4; Length 22073;
 Best Local Similarity 58.7%; Pred. No. 5.5e+02;
 RESULT 931
 ID ABL97570 standard; DNA; 22073 BP.
 DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2222.
 PN WO200155317-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 4.1%; Score 31.2; DB 4; Length 22073;
 Best Local Similarity 58.7%; Pred. No. 5.5e+02;
 RESULT 932
 ID ABZ74560 standard; DNA; 22073 BP.
 DE Secreted protein gene 351 genomic fragment HTXDB22, SEQ ID NO:1707.
 PN WO200277013-A2.
 PD 03-OCT-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 4.1%; Score 31.2; DB 8; Length 22073;
 Best Local Similarity 58.7%; Pred. No. 5.5e+02;
 RESULT 933
 ID ABZ68092 standard; DNA; 22073 BP.
 DE Human secreted protein encoding genomic DNA SEQ ID NO 1615.
 PN WO200277186-A2.
 PD 03-OCT-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 4.1%; Score 31.2; DB 10; Length 22073;
 Best Local Similarity 58.7%; Pred. No. 5.5e+02;
 RESULT 934
 ID ABL09362 standard; cDNA; 24066 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 22568.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 4.1%; Score 31.2; DB 4; Length 24066;
 Best Local Similarity 51.4%; Pred. No. 5.8e+02;
 RESULT 935
 ID ABL09362 standard; cDNA; 24066 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 22568.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 4.1%; Score 31.2; DB 4; Length 24066;
 Best Local Similarity 51.4%; Pred. No. 5.8e+02;
 RESULT 936
 ID ABL09362 standard; cDNA; 24066 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 22568.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 4.1%; Score 31.2; DB 4; Length 24066;
 Best Local Similarity 51.4%; Pred. No. 5.8e+02;
 RESULT 937
 ID ABL09362 standard; cDNA; 24066 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 22568.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 4.1%; Score 31.2; DB 4; Length 24066;
 Best Local Similarity 51.4%; Pred. No. 5.8e+02;
 RESULT 938
 ID ABL09362 standard; cDNA; 24066 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 22568.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 4.1%; Score 31.2; DB 4; Length 24066;
 Best Local Similarity 51.4%; Pred. No. 5.8e+02;
 RESULT 939
 ID ABL09362 standard; cDNA; 24066 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 22568.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 4.1%; Score 31.2; DB 4; Length 24066;
 Best Local Similarity 51.4%; Pred. No. 5.8e+02;
 RESULT 940
 ID ABL09362 standard; cDNA; 24066 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 22568.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 4.1%; Score 31.2; DB 4; Length 24066;
 Best Local Similarity 51.4%; Pred. No. 5.8e+02;
 RESULT 941
 ID ABL09362 standard; cDNA; 24066 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 22568.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 4.1%; Score 31.2; DB 4; Length 24066;
 Best Local Similarity 51.4%; Pred. No. 5.8e+02;
 RESULT 942
 ID ABL09362 standard; cDNA; 24066 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 22568.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 4.1%; Score 31.2; DB 4; Length 24066;
 Best Local Similarity 51.4%; Pred. No. 5.8e+02;
 RESULT 943
 ID ABL09362 standard; cDNA; 24066 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 22568.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 4.1%; Score 31.2; DB 4; Length 24066;
 Best Local Similarity 51.4%; Pred. No. 5.8e+02;
 RESULT 944
 ID ABL09362 standard; cDNA; 24066 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 22568.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 4.1%; Score 31.2; DB 4; Length 24066;
 Best Local Similarity 51.4%; Pred. No. 5.8e+02;
 RESULT 945
 ID ABL09362 standard; cDNA; 24066 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 22568.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 4.1%; Score 31.2; DB 4; Length 24066;
 Best Local Similarity 51.4%; Pred. No. 5.8e+02;
 RESULT 946

Query Match 4.1%; Score 31.2; DB 12; Length 110000;
 Best Local Similarity 47.9%; Pred. No. 1.2e+03;
 RESULT 947
 ID ADL08109 standard; DNA; 247682 BP.
 DE Human gene associated with low HDL-C AT3.
 PN US2004043389-A1.
 PD 04-MAR-2004.
 PA (VITI-) VITIVITY INC.
 Query Match 4.1%; Score 31.2; DB 12; Length 247682;
 Best Local Similarity 47.9%; Pred. No. 1.6e+03;
 RESULT 948
 ID ABK89296 standard; DNA; 326014 BP.
 DE Human gene for novel serine/threonine serine kinase.
 Query Match 4.1%; Score 31.2; DB 6; Length 326014;
 Best Local Similarity 60.7%; Pred. No. 1.8e+03;
 RESULT 949
 ID ADQ94981 standard; DNA; 326014 BP.
 DE Human kinase genomic DNA.
 Query Match 4.1%; Score 31.2; DB 12; Length 326014;
 Best Local Similarity 60.7%; Pred. No. 1.8e+03;
 RESULT 950
 ID AAC29772 standard; cDNA; 389 BP.
 DE Human secreted protein 5' EST, SEQ ID NO: 33847.
 PN EP1033401-A2.
 PD 06-SEP-2000.
 PA (GEST) GENSET.
 Query Match 4.0%; Score 31; DB 3; Length 389;
 Best Local Similarity 57.9%; Pred. No. 96;
 RESULT 951
 ID ABV06585 standard; cDNA; 393 BP.
 DE Human prostate expression marker cDNA 6576.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 4.0%; Score 31; DB 5; Length 393;
 Best Local Similarity 52.8%; Pred. No. 97;
 RESULT 952
 ID ABX62061 standard; DNA; 429 BP.
 DE Arabidopsis thaliana expressed sequence related polynucleotide #176.
 PN US2002040490-A1.
 PD 04-APR-2002.
 PA (GORL/) GORLACH J.
 PA (ANYI/) AN Y.
 PA (HAMI/) HAMILTON C M.
 PA (PRIC/) PRICE J L.
 PA (RAIN/) RAINES T M.
 PA (YUYI/) YU Y.
 PA (RAME/) RAMEAKA J G.
 PA (PAGE/) PAGE A.
 PA (MATH/) MATHW A V.
 PA (LEDF/) LEDFORD B L.
 PA (WOES/) WOESSNER J P.
 PA (HAAS/) HAAS W D.
 PA (GARC/) GARCIA C A.
 PA (KRIC/) KRICKER M.
 PA (SLAT/) SLATER T.
 PA (DAVI/) DAVIS K R.
 PA (ALLE/) ALLEN K.
 PA (HOFF/) HOFFMAN N.
 PA (HURB/) HURBAN P.
 Query Match 4.0%; Score 31; DB 5; Length 429;
 Best Local Similarity 52.8%; Pred. No. 97;
 RESULT 953
 ID AAF12938 standard; cDNA; 636 BP.
 DE Aspergillus oryzae EST SEQ ID NO:5461.
 PN WO200056762-A2.
 PD 28-SEP-2000.
 PA (NOVO) NOVO NORDISK BIOTECH INC.
 PA (NOVO) NOVO NORDISK AS.
 Query Match 4.0%; Score 31; DB 3; Length 636;
 Best Local Similarity 51.0%; Pred. No. 1.2e+02;
 RESULT 954
 ID ADN73602 standard; cDNA; 648 BP.

DE Thale cress cDNA repressed in E2Fa/Dpa expressing plants SeqID 1497.
 PN WO2004035798-A2.
 PD 29-APR-2004.
 PA (CROP-) CROPDISEIGN NV.
 Query Match 4.0%; Score 31; DB 12; Length 648;
 Best Local Similarity 59.8%; Pred. No. 1.2e+02;
 RESULT 955
 ID ABN99075 standard; DNA; 792 BP.
 DE Arabidopsis thaliana expressed polynucleotide SEQ ID NO 843.
 PN US2002023281-A1.
 PD 21-FEB-2002.
 PA (GORL/) GORLACH J.
 PA (ANYI/) AN Y.
 PA (HAMI/) HAMILTON C M.
 PA (PRIC/) PRICE J L.
 PA (RAIN/) RAINES T M.
 PA (YUYI/) YU Y.
 PA (RAME/) RAMEAKA J G.
 PA (PAGE/) PAGE A.
 PA (MATH/) MATHW A V.
 PA (LEDF/) LEDFORD B L.
 PA (WOES/) WOESSNER J P.
 PA (HAAS/) HAAS W D.
 PA (GARC/) GARCIA C A.
 PA (KRIC/) KRICKER M.
 PA (SLAT/) SLATER T.
 PA (DAVI/) DAVIS K R.
 PA (ALLE/) ALLEN K.
 PA (HOFF/) HOFFMAN N.
 PA (HURB/) HURBAN P.
 Query Match 4.0%; Score 31; DB 6; Length 792;
 Best Local Similarity 59.8%; Pred. No. 1.3e+02;
 RESULT 956
 ID AAA02568 standard; cDNA; 1347 BP.
 DE Human colon cancer cell line polynucleotide sequence SEQ ID NO:2559.
 PN WO9958675-A2.
 PD 18-NOV-1999.
 PA (CHIR) CHIRON CORP.
 PA (HYSE-) HYSEQ INC.
 Query Match 4.0%; Score 31; DB 3; Length 1347;
 Best Local Similarity 42.1%; Pred. No. 1.7e+02;
 RESULT 957
 ID ABN66457 standard; DNA; 1353 BP.
 DE Streptococcus polynucleotide SEQ ID NO 827.
 PN WO200234771-A2.
 PD 02-MAY-2002.
 PA (CHIR-) CHIRON SPA.
 PA (GENO-) INST GENOMIC RES.
 Query Match 4.0%; Score 31; DB 6; Length 1353;
 Best Local Similarity 51.0%; Pred. No. 1.7e+02;
 RESULT 958
 ID ABL22302 standard; DNA; 2899 BP.
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 18379.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 4.0%; Score 31; DB 4; Length 2899;
 Best Local Similarity 46.5%; Pred. No. 2.5e+02;
 RESULT 959
 ID ABL28608 standard; DNA; 2985 BP.
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 37297.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 4.0%; Score 31; DB 4; Length 2985;
 Best Local Similarity 46.5%; Pred. No. 2.5e+02;
 RESULT 960
 ID AAL41291 standard; cDNA; 3051 BP.
 DE cDNA encoding the protein EST1-1089.
 PN EP1245671-A1.
 PD 02-OCT-2002.
 PA (BTGI-) BTG INT LTD.
 Query Match 4.0%; Score 31; DB 6; Length 3051;

Best Local Similarity 57.9%; Pred. No. 2.5e+02;
 RESULT 961
 ID ABV72520 standard; cDNA; 3051 BP.
 DE Nucleotide sequence of a human protein designated EST1-1089.
 PN WO200277220-A2.
 PD 03-OCT-2002.
 PA (BTGI-) BTG INT LTD.
 Query Match 4.0%; Score 31; DB 8; Length 3051;
 Best Local Similarity 57.9%; Pred. No. 2.5e+02;
 RESULT 962
 ID ABL08882 standard; cDNA; 3658 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 21128.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 4.0%; Score 31; DB 4; Length 3658;
 Best Local Similarity 59.8%; Pred. No. 2.7e+02;
 RESULT 963
 ID AAF29637 standard; DNA; 5429 BP.
 DE Arabidopsis thaliana fwa gene.
 PN WO200102573-A1.
 PD 11-JAN-2001.
 PA (UYWA-) UNIV WAGENINGEN.
 Query Match 4.0%; Score 31; DB 5; Length 5429;
 Best Local Similarity 50.3%; Pred. No. 3.3e+02;
 RESULT 964
 ID AAF29556 standard; DNA; 5429 BP.
 DE Arabidopsis thaliana ecotype Landsberg erecta FWA-1 gene.
 PN WO200102572-A1.
 PD 11-JAN-2001.
 PA (UYWA-) UNIV WAGENINGEN.
 Query Match 4.0%; Score 31; DB 5; Length 5429;
 Best Local Similarity 50.3%; Pred. No. 3.3e+02;
 RESULT 965
 ID ARA19876 standard; DNA; 8588 BP.
 DE Human nervous system related polynucleotide SEQ ID NO 12207.
 PN WO200159063-A2.
 PD 16-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 4.0%; Score 31; DB 5; Length 8588;
 Best Local Similarity 50.3%; Pred. No. 4.1e+02;
 RESULT 966
 ID ARA16043 standard; DNA; 8588 BP.
 DE Human nervous system related polynucleotide SEQ ID NO 8374.
 PN WO200159063-A2.
 PD 16-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 4.0%; Score 31; DB 5; Length 8588;
 Best Local Similarity 50.3%; Pred. No. 4.1e+02;
 RESULT 967
 ID AAD62832 standard; DNA; 180216 BP.
 DE Human BAC #1 containing formin (fmm)-2 genomic DNA.
 PN US2003170683-A1.
 PD 11-SEP-2003.
 PA (LEDE/) LEADER P.
 PA (LEAD/) LEADER B.
 Query Match 4.0%; Score 31; DB 10; Length 180216;
 Best Local Similarity 49.1%; Pred. No. 1.6e+03;
 RESULT 969
 ID ABV15242 standard; cDNA; 265 BP.
 DE Human prostate expression marker cDNA 15233.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 4.0%; Score 30.8; DB 5; Length 265;
 Best Local Similarity 53.3%; Pred. No. 92;
 RESULT 970
 ID ABV06073 standard; cDNA; 285 BP.
 DE Human prostate expression marker cDNA 6064.
 PN WO200160860-A2.

PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 4.0%; Score 30.8; DB 5; Length 285;
 Best Local Similarity 53.3%; Pred. No. 96;
 RESULT 971
 ID ABV02501 standard; cDNA; 303 BP.
 DE Human prostate expression marker cDNA 2492.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 4.0%; Score 30.8; DB 5; Length 303;
 Best Local Similarity 53.3%; Pred. No. 98;
 RESULT 972
 ID ABV06050 standard; cDNA; 323 BP.
 DE Human prostate expression marker cDNA 6041.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 4.0%; Score 30.8; DB 5; Length 323;
 Best Local Similarity 53.3%; Pred. No. 1e+02;
 RESULT 973
 ID ABV00225 standard; cDNA; 327 BP.
 DE Human prostate expression marker cDNA 216.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 4.0%; Score 30.8; DB 5; Length 327;
 Best Local Similarity 53.3%; Pred. No. 1e+02;
 RESULT 974
 ID ABV00462 standard; cDNA; 328 BP.
 DE Human prostate expression marker cDNA 453.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 4.0%; Score 30.8; DB 5; Length 328;
 Best Local Similarity 53.3%; Pred. No. 1e+02;
 RESULT 975
 ID ABV11345 standard; cDNA; 331 BP.
 DE Human prostate expression marker cDNA 11336.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 4.0%; Score 30.8; DB 5; Length 331;
 Best Local Similarity 53.3%; Pred. No. 1e+02;
 RESULT 976
 ID ABV15219 standard; cDNA; 341 BP.
 DE Human prostate expression marker cDNA 15210.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 4.0%; Score 30.8; DB 5; Length 341;
 Best Local Similarity 53.3%; Pred. No. 1e+02;
 RESULT 977
 ID ABV07323 standard; cDNA; 344 BP.
 DE Human prostate expression marker cDNA 7314.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 4.0%; Score 30.8; DB 5; Length 344;
 Best Local Similarity 53.3%; Pred. No. 1e+02;
 RESULT 978
 ID ABV15215 standard; cDNA; 346 BP.
 DE Human prostate expression marker cDNA 15206.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 4.0%; Score 30.8; DB 5; Length 346;
 Best Local Similarity 53.3%; Pred. No. 1e+02;
 RESULT 979
 ID ABV09631 standard; cDNA; 346 BP.
 DE Human prostate expression marker cDNA 9622.
 PN WO200160860-A2.
 PD 23-AUG-2001.

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 346;
Best Local Similarity 53.3%; Pred. No. 1.e+02;
RESULT 980
ID ABV02913 standard; cDNA; 355 BP.
DE Human prostate expression marker cDNA 2904.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 355;
Best Local Similarity 53.3%; Pred. No. 1.e+02;
RESULT 981
ID ABV12082 standard; cDNA; 356 BP.
DE Human prostate expression marker cDNA 12073.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 356;
Best Local Similarity 53.3%; Pred. No. 1.e+02;
RESULT 982
ID ABV10258 standard; cDNA; 361 BP.
DE Human prostate expression marker cDNA 10249.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 361;
Best Local Similarity 53.3%; Pred. No. 1.e+02;
RESULT 983
ID ABV02365 standard; cDNA; 362 BP.
DE Human prostate expression marker cDNA 2356.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 362;
Best Local Similarity 53.3%; Pred. No. 1.e+02;
RESULT 984
ID ABV06786 standard; cDNA; 363 BP.
DE Human prostate expression marker cDNA 6777.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 363;
Best Local Similarity 53.3%; Pred. No. 1.e+02;
RESULT 985
ID ABV09020 standard; cDNA; 366 BP.
DE Human prostate expression marker cDNA 9011.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 366;
Best Local Similarity 53.3%; Pred. No. 1.e+02;
RESULT 986
ID ABV11534 standard; cDNA; 372 BP.
DE Human prostate expression marker cDNA 11525.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 372;
Best Local Similarity 53.3%; Pred. No. 1.e+02;
RESULT 987
ID ABV11804 standard; cDNA; 374 BP.
DE Human prostate expression marker cDNA 11795.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 374;
Best Local Similarity 53.3%; Pred. No. 1.e+02;
RESULT 988
ID ABV11780 standard; cDNA; 374 BP.
DE Human prostate expression marker cDNA 11771.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 385;
Best Local Similarity 53.3%; Pred. No. 1.e+02;
RESULT 989
ID ABV12165 standard; cDNA; 374 BP.
DE Human prostate expression marker cDNA 12156.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 374;
Best Local Similarity 53.3%; Pred. No. 1.e+02;
RESULT 990
ID ABV10423 standard; cDNA; 376 BP.
DE Human prostate expression marker cDNA 10414.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 376;
Best Local Similarity 53.3%; Pred. No. 1.e+02;
RESULT 991
ID ABV02635 standard; cDNA; 380 BP.
DE Human prostate expression marker cDNA 2626.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 380;
Best Local Similarity 53.3%; Pred. No. 1.e+02;
RESULT 992
ID ABV10172 standard; cDNA; 381 BP.
DE Human prostate expression marker cDNA 10163.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 381;
Best Local Similarity 53.3%; Pred. No. 1.e+02;
RESULT 993
ID ABV02732 standard; cDNA; 381 BP.
DE Human prostate expression marker cDNA 2723.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 381;
Best Local Similarity 53.3%; Pred. No. 1.e+02;
RESULT 994
ID ABV36014 standard; cDNA; 383 BP.
DE Human prostate expression marker cDNA 36005.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 383;
Best Local Similarity 53.3%; Pred. No. 1.e+02;
RESULT 995
ID ABV32490 standard; cDNA; 383 BP.
DE Human prostate expression marker cDNA 32481.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 383;
Best Local Similarity 53.3%; Pred. No. 1.e+02;
RESULT 996
ID ABV11707 standard; cDNA; 383 BP.
DE Human prostate expression marker cDNA 11698.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 383;
Best Local Similarity 53.3%; Pred. No. 1.e+02;
RESULT 997
ID ABV11541 standard; cDNA; 385 BP.
DE Human prostate expression marker cDNA 11532.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 385;

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Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 998
ID ABV32815 standard; cDNA; 385 BP.
DE Human prostate expression marker cDNA 32806.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 385;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 999
ID ABV10522 standard; cDNA; 388 BP.
DE Human prostate expression marker cDNA 10513.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 388;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1000
ID ABV02996 standard; cDNA; 390 BP.
DE Human prostate expression marker cDNA 2987.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 390;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1001
ID ABV11670 standard; cDNA; 391 BP.
DE Human prostate expression marker cDNA 11661.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 391;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1002
ID ABV1899 standard; cDNA; 391 BP.
DE Human prostate expression marker cDNA 11890.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 391;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1003
ID ABV02734 standard; cDNA; 391 BP.
DE Human prostate expression marker cDNA 2725.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 391;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1004
ID ABV31270 standard; cDNA; 392 BP.
DE Human prostate expression marker cDNA 31261.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 392;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1005
ID ABV11903 standard; cDNA; 393 BP.
DE Human prostate expression marker cDNA 11894.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 393;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1006
ID ABV15400 standard; cDNA; 395 BP.
DE Human prostate expression marker cDNA 15391.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 395;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1007
ID ABV11821 standard; cDNA; 396 BP.
DE Human prostate expression marker cDNA 11812.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 396;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1008
ID ABV11947 standard; cDNA; 397 BP.
DE Human prostate expression marker cDNA 11938.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 397;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1009
ID ABV11555 standard; cDNA; 398 BP.
DE Human prostate expression marker cDNA 11546.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 398;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1010
ID ABV11901 standard; cDNA; 398 BP.
DE Human prostate expression marker cDNA 11892.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 398;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1011
ID ABV12026 standard; cDNA; 399 BP.
DE Human prostate expression marker cDNA 12017.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 399;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1012
ID ABV02814 standard; cDNA; 400 BP.
DE Human prostate expression marker cDNA 2805.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 400;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1013
ID ABV32679 standard; cDNA; 401 BP.
DE Human prostate expression marker cDNA 32670.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 401;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1014
ID ABV11712 standard; cDNA; 401 BP.
DE Human prostate expression marker cDNA 11703.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 401;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1015
ID ABV43873 standard; cDNA; 402 BP.
DE Human prostate expression marker cDNA 43864.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 402;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1016

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ID ABV02909 standard; cDNA; 402 BP.
DE Human prostate expression marker cDNA 2900.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 402;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1017
ID ABV31429 standard; cDNA; 402 BP.
DE Human prostate expression marker cDNA 31420.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 402;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1018
ID ABV11983 standard; cDNA; 402 BP.
DE Human prostate expression marker cDNA 11974.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 402;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1019
ID ABV02538 standard; cDNA; 406 BP.
DE Human prostate expression marker cDNA 2529.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 406;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1020
ID ABV11825 standard; cDNA; 406 BP.
DE Human prostate expression marker cDNA 11816.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 406;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1021
ID ABV33227 standard; cDNA; 407 BP.
DE Human prostate expression marker cDNA 33218.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 407;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1022
ID ABV42150 standard; cDNA; 407 BP.
DE Human prostate expression marker cDNA 42141.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 407;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1023
ID ABV02386 standard; cDNA; 407 BP.
DE Human prostate expression marker cDNA 2377.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 407;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1024
ID ABV12163 standard; cDNA; 410 BP.
DE Human prostate expression marker cDNA 12154.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 410;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1025
ID ABV10237 standard; cDNA; 410 BP.
DE Human prostate expression marker cDNA 10228.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 410;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1026
ID ABV36018 standard; cDNA; 411 BP.
DE Human prostate expression marker cDNA 36009.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 411;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1027
ID ABV06231 standard; cDNA; 411 BP.
DE Human prostate expression marker cDNA 6222.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 411;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1028
ID ABV32925 standard; cDNA; 414 BP.
DE Human prostate expression marker cDNA 32916.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 414;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1029
ID ABV41850 standard; cDNA; 414 BP.
DE Human prostate expression marker cDNA 41841.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 414;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1030
ID ABV32852 standard; cDNA; 416 BP.
DE Human prostate expression marker cDNA 32843.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 416;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1031
ID ABV02857 standard; cDNA; 416 BP.
DE Human prostate expression marker cDNA 2848.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 416;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1032
ID ABV02730 standard; cDNA; 417 BP.
DE Human prostate expression marker cDNA 2721.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 417;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1033
ID ABV33310 standard; cDNA; 418 BP.
DE Human prostate expression marker cDNA 33301.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 418;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1034
ID ABV42233 standard; cDNA; 418 BP.
DE Human prostate expression marker cDNA 42224.

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PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match
  Best Local Similarity 53.3%; Score 30.8; DB 5; Length 418;
  RESULT 1035
  ID ABV45074 standard; cDNA; 419 BP.
  DE Human prostate expression marker cDNA 45065.
  PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match
  Best Local Similarity 53.3%; Score 30.8; DB 5; Length 419;
  RESULT 1036
  ID ABV01003 standard; cDNA; 419 BP.
  DE Human prostate expression marker cDNA 994.
  PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match
  Best Local Similarity 53.3%; Score 30.8; DB 5; Length 419;
  RESULT 1037
  ID ABV31593 standard; cDNA; 419 BP.
  DE Human prostate expression marker cDNA 31584.
  PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match
  Best Local Similarity 53.3%; Score 30.8; DB 5; Length 419;
  RESULT 1038
  ID ABV32886 standard; cDNA; 419 BP.
  DE Human prostate expression marker cDNA 32677.
  PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match
  Best Local Similarity 53.3%; Score 30.8; DB 5; Length 419;
  RESULT 1039
  ID ABV41777 standard; cDNA; 419 BP.
  DE Human prostate expression marker cDNA 41768.
  PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match
  Best Local Similarity 53.3%; Score 30.8; DB 5; Length 419;
  RESULT 1040
  ID ABV32949 standard; cDNA; 421 BP.
  DE Human prostate expression marker cDNA 32940.
  PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match
  Best Local Similarity 53.3%; Score 30.8; DB 5; Length 421;
  RESULT 1041
  ID ABV01254 standard; cDNA; 421 BP.
  DE Human prostate expression marker cDNA 1245.
  PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match
  Best Local Similarity 53.3%; Score 30.8; DB 5; Length 421;
  RESULT 1042
  ID ABV12282 standard; cDNA; 422 BP.
  DE Human prostate expression marker cDNA 12273.
  PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match
  Best Local Similarity 53.3%; Score 30.8; DB 5; Length 422;
  RESULT 1043
  ID ABV31343 standard; cDNA; 422 BP.
  DE Human prostate expression marker cDNA 31334.
  PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match
  Best Local Similarity 53.3%; Score 30.8; DB 5; Length 422;
  RESULT 1044
  ID ABV02652 standard; cDNA; 423 BP.
  DE Human prostate expression marker cDNA 2643.
  PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match
  Best Local Similarity 53.3%; Score 30.8; DB 5; Length 423;
  RESULT 1045
  ID ABK39114 standard; cDNA; 427 BP.
  DE cDNA encoding lung tumour protein clone R0130:G12.
  PN WO200204514-A2.
PD 17-JAN-2002.
PA (CORI-) CORIXA CORP.
  Query Match
  Best Local Similarity 53.3%; Score 30.8; DB 6; Length 427;
  RESULT 1046
  ID ACA11443 standard; cDNA; 427 BP.
  DE Human lung adenocarcinoma library cDNA SEQ ID 1152.
  PN US2002197669-A1.
PD 26-DEC-2002.
PA (BANG/) BANGUR C S.
PA (FANG/) FANGER G R.
PA (WANG/) WANG A.
PA (WANG/) WANG T.
PA (SWIT/) SWITZER A P.
PA (MCNE/) MCNEILL P D.
PA (CLAP/) CLAPPER J D.
  Query Match
  Best Local Similarity 66.7%; Score 30.8; DB 8; Length 427;
  RESULT 1047
  ID ACA02629 standard; cDNA; 427 BP.
  DE Lung cancer therapy and diagnosis associated cDNA #1118.
  PN US2002172952-A1.
PD 21-NOV-2002.
PA (CORI-) CORIXA CORP.
  Query Match
  Best Local Similarity 66.7%; Score 30.8; DB 8; Length 427;
  RESULT 1048
  ID ADH46671 standard; cDNA; 427 BP.
  DE Human lung tumour cDNA clone, SEQ ID No 1152.
  PN WO2003037267-A2.
PD 08-MAY-2003.
PA (CORI-) CORIXA CORP.
  Query Match
  Best Local Similarity 66.7%; Score 30.8; DB 10; Length 427;
  RESULT 1049
  ID ABV33044 standard; cDNA; 428 BP.
  DE Human prostate expression marker cDNA 33035.
  PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match
  Best Local Similarity 53.3%; Score 30.8; DB 5; Length 428;
  RESULT 1050
  ID ABV41969 standard; cDNA; 428 BP.
  DE Human prostate expression marker cDNA 41960.
  PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match
  Best Local Similarity 53.3%; Score 30.8; DB 5; Length 428;
  RESULT 1051
  ID ABV02974 standard; cDNA; 429 BP.
  DE Human prostate expression marker cDNA 2965.
  PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match
  Best Local Similarity 53.3%; Score 30.8; DB 5; Length 429;
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Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1052
ID ABV03113 standard; cDNA; 429 BP.
DE Human prostate expression marker cDNA 3104.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 429;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1053
ID ABV12143 standard; cDNA; 430 BP.
DE Human prostate expression marker cDNA 12134.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 430;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1054
ID ABV12193 standard; cDNA; 432 BP.
DE Human prostate expression marker cDNA 12184.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 432;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1055
ID ABV33048 standard; cDNA; 432 BP.
DE Human prostate expression marker cDNA 33039.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 432;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1056
ID ABV32966 standard; cDNA; 434 BP.
DE Human prostate expression marker cDNA 32957.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 434;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1057
ID ABV31692 standard; cDNA; 434 BP.
DE Human prostate expression marker cDNA 31683.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 434;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1058
ID ABV03024 standard; cDNA; 435 BP.
DE Human prostate expression marker cDNA 3015.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 435;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1059
ID ABV32857 standard; cDNA; 435 BP.
DE Human prostate expression marker cDNA 32848.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 435;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1060
ID ABV42053 standard; cDNA; 435 BP.
DE Human prostate expression marker cDNA 42044.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 435;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1061
ID ABV33128 standard; cDNA; 435 BP.
DE Human prostate expression marker cDNA 33119.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 435;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1062
ID ABV07053 standard; cDNA; 438 BP.
DE Human prostate expression marker cDNA 7044.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 438;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1063
ID ABV36192 standard; cDNA; 439 BP.
DE Human prostate expression marker cDNA 36183.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 439;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1064
ID ABV45244 standard; cDNA; 439 BP.
DE Human prostate expression marker cDNA 45235.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 439;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1065
ID ABV33092 standard; cDNA; 440 BP.
DE Human prostate expression marker cDNA 33083.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 440;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1066
ID ABV42017 standard; cDNA; 440 BP.
DE Human prostate expression marker cDNA 42008.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 440;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1067
ID ABV41782 standard; cDNA; 440 BP.
DE Human prostate expression marker cDNA 41773.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 440;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1068
ID ABV36995 standard; cDNA; 441 BP.
DE Human prostate expression marker cDNA 36986.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 441;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1069
ID ABV41874 standard; cDNA; 441 BP.
DE Human prostate expression marker cDNA 41865.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 441;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1070
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ID ABV02372 standard; cDNA; 441 BP.
DE Human prostate expression marker cDNA 2363.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1071 Length 441;
ID ABV36732 standard; cDNA; 442 BP.
DE Human prostate expression marker cDNA 36723.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1072 Length 442;
ID ABV32700 standard; cDNA; 443 BP.
DE Human prostate expression marker cDNA 32691.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1073 Length 443;
ID ABV41740 standard; cDNA; 443 BP.
DE Human prostate expression marker cDNA 41731.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1074 Length 443;
ID ABV41805 standard; cDNA; 443 BP.
DE Human prostate expression marker cDNA 41796.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1075 Length 443;
ID ABV02778 standard; cDNA; 445 BP.
DE Human prostate expression marker cDNA 2769.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1076 Length 445;
ID ABV42095 standard; cDNA; 446 BP.
DE Human prostate expression marker cDNA 42086.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1077 Length 446;
ID ABV41846 standard; cDNA; 446 BP.
DE Human prostate expression marker cDNA 41837.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1078 Length 446;
ID ABV31171 standard; cDNA; 446 BP.
DE Human prostate expression marker cDNA 33162.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1079 Length 446;
ID ABV32970 standard; cDNA; 447 BP.

DE Human prostate expression marker cDNA 32961.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1080 Length 447;
ID ABV02656 standard; cDNA; 450 BP.
DE Human prostate expression marker cDNA 2647.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1081 Length 450;
ID ABV31408 standard; cDNA; 452 BP.
DE Human prostate expression marker cDNA 31399.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1082 Length 452;
ID ABV40377 standard; cDNA; 452 BP.
DE Human prostate expression marker cDNA 40368.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1083 Length 452;
ID ABV01068 standard; cDNA; 453 BP.
DE Human prostate expression marker cDNA 1059.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1084 Length 453;
ID ABV33427 standard; cDNA; 462 BP.
DE Human prostate expression marker cDNA 33418.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1085 Length 462;
ID ABV33308 standard; cDNA; 463 BP.
DE Human prostate expression marker cDNA 33299.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1086 Length 463;
ID ABV33288 standard; cDNA; 464 BP.
DE Human prostate expression marker cDNA 33279.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1087 Length 464;
ID ABV40312 standard; cDNA; 464 BP.
DE Human prostate expression marker cDNA 40303.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1088 Length 464;
ID ABV40561 standard; cDNA; 464 BP.
DE Human prostate expression marker cDNA 40552.

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PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 53.3%; Pred. No. 1.2e+02; Length 464;
RESULT 1099
ID ABV40660 standard; cDNA; 464 BP.
DE Human prostate expression marker cDNA 40651.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 53.3%; Pred. No. 1.2e+02; Length 464;
RESULT 1090
ID ABV45053 standard; cDNA; 464 BP.
DE Human prostate expression marker cDNA 45044.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 53.3%; Pred. No. 1.2e+02; Length 464;
RESULT 1091
ID ABV42211 standard; cDNA; 464 BP.
DE Human prostate expression marker cDNA 42202.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 53.3%; Pred. No. 1.2e+02; Length 464;
RESULT 1092
ID ABV40398 standard; cDNA; 468 BP.
DE Human prostate expression marker cDNA 40389.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 53.3%; Pred. No. 1.2e+02; Length 468;
RESULT 1093
ID ABV3338 standard; cDNA; 468 BP.
DE Human prostate expression marker cDNA 33329.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 53.3%; Pred. No. 1.2e+02; Length 468;
RESULT 1094
ID ABV45078 standard; cDNA; 469 BP.
DE Human prostate expression marker cDNA 45069.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 53.3%; Pred. No. 1.2e+02; Length 469;
RESULT 1095
ID ABV33443 standard; cDNA; 469 BP.
DE Human prostate expression marker cDNA 33434.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 53.3%; Pred. No. 1.2e+02; Length 469;
RESULT 1096
ID ABV42366 standard; cDNA; 469 BP.
DE Human prostate expression marker cDNA 42357.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 53.3%; Pred. No. 1.2e+02; Length 469;
RESULT 1097
ID ABV06651 standard; cDNA; 496 BP.
DE Human prostate expression marker cDNA 6642.
PN WO200160860-A2.

PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 53.3%; Pred. No. 1.2e+02; Length 496;
RESULT 1098
ID ABV60369 standard; cDNA; 504 BP.
DE Human prostate expression marker cDNA 60360.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 53.3%; Pred. No. 1.2e+02; Length 504;
RESULT 1099
ID ABV39172 standard; cDNA; 517 BP.
DE Human prostate expression marker cDNA 39163.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 53.3%; Pred. No. 1.3e+02; Length 517;
RESULT 1100
ID ABV36599 standard; cDNA; 520 BP.
DE Human prostate expression marker cDNA 36590.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 53.3%; Pred. No. 1.3e+02; Length 520;
RESULT 1101
ID ABV41604 standard; cDNA; 520 BP.
DE Human prostate expression marker cDNA 41595.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 53.3%; Pred. No. 1.3e+02; Length 520;
RESULT 1102
ID ABV06802 standard; cDNA; 541 BP.
DE Human prostate expression marker cDNA 6793.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 53.3%; Pred. No. 1.3e+02; Length 541;
RESULT 1103
ID ABV02706 standard; cDNA; 565 BP.
DE Human prostate expression marker cDNA 2697.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 53.3%; Pred. No. 1.3e+02; Length 565;
RESULT 1104
ID ABV03129 standard; cDNA; 569 BP.
DE Human prostate expression marker cDNA 3120.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 53.3%; Pred. No. 1.3e+02; Length 569;
RESULT 1105
ID ADI72125 standard; DNA; 578 BP.
DE Human ovarian cancer DNA marker #4867.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 41.3%; Pred. No. 1.3e+02; Length 578;
RESULT 1106
ID ADI37274 standard; DNA; 578 BP.
DE Human ovarian cancer DNA marker #11164.
PN WO200170979-A2.
PD 27-SEP-2001.

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PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 578;
Best Local Similarity 41.3%; Pred. No. 1.3e+02;
RESULT 1107
ID ABV42146 standard; cDNA; 602 BP.
DE Human prostate expression marker cDNA 42137.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 602;
Best Local Similarity 53.3%; Pred. No. 1.4e+02;
RESULT 1108
ID ABV41895 standard; cDNA; 602 BP.
DE Human prostate expression marker cDNA 41886.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 602;
Best Local Similarity 53.3%; Pred. No. 1.4e+02;
RESULT 1109
ID ABV39454 standard; cDNA; 602 BP.
DE Human prostate expression marker cDNA 39445.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 602;
Best Local Similarity 53.3%; Pred. No. 1.4e+02;
RESULT 1110
ID ABV37259 standard; cDNA; 602 BP.
DE Human prostate expression marker cDNA 37250.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 602;
Best Local Similarity 53.3%; Pred. No. 1.4e+02;
RESULT 1111
ID ABV36748 standard; cDNA; 602 BP.
DE Human prostate expression marker cDNA 36739.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 602;
Best Local Similarity 53.3%; Pred. No. 1.4e+02;
RESULT 1112
ID ABV41891 standard; cDNA; 602 BP.
DE Human prostate expression marker cDNA 41882.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 602;
Best Local Similarity 53.3%; Pred. No. 1.4e+02;
RESULT 1113
ID ABV41419 standard; cDNA; 602 BP.
DE Human prostate expression marker cDNA 41410.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 602;
Best Local Similarity 53.3%; Pred. No. 1.4e+02;
RESULT 1114
ID ABV43273 standard; cDNA; 602 BP.
DE Human prostate expression marker cDNA 43264.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 602;
Best Local Similarity 53.3%; Pred. No. 1.4e+02;
RESULT 1115
ID ABV33046 standard; cDNA; 602 BP.
DE Human prostate expression marker cDNA 33037.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 689;
Best Local Similarity 53.3%; Pred. No. 1.4e+02;
RESULT 1116
ID ABV41973 standard; cDNA; 602 BP.
DE Human prostate expression marker cDNA 41964.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 602;
Best Local Similarity 53.3%; Pred. No. 1.4e+02;
RESULT 1117
ID ABV42261 standard; cDNA; 602 BP.
DE Human prostate expression marker cDNA 42252.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 602;
Best Local Similarity 53.3%; Pred. No. 1.4e+02;
RESULT 1118
ID ABV41971 standard; cDNA; 602 BP.
DE Human prostate expression marker cDNA 41962.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 602;
Best Local Similarity 53.3%; Pred. No. 1.4e+02;
RESULT 1119
ID ABV41611 standard; cDNA; 602 BP.
DE Human prostate expression marker cDNA 41602.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 602;
Best Local Similarity 53.3%; Pred. No. 1.4e+02;
RESULT 1120
ID ABV42231 standard; cDNA; 602 BP.
DE Human prostate expression marker cDNA 42222.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 602;
Best Local Similarity 53.3%; Pred. No. 1.4e+02;
RESULT 1121
ID ABV42350 standard; cDNA; 602 BP.
DE Human prostate expression marker cDNA 42341.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 602;
Best Local Similarity 53.3%; Pred. No. 1.4e+02;
RESULT 1122
ID ABV41625 standard; cDNA; 602 BP.
DE Human prostate expression marker cDNA 41616.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 602;
Best Local Similarity 53.3%; Pred. No. 1.4e+02;
RESULT 1123
ID ABV09048 standard; cDNA; 603 BP.
DE Human prostate expression marker cDNA 9039.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 603;
Best Local Similarity 53.3%; Pred. No. 1.4e+02;
RESULT 1124
ID ABV12298 standard; cDNA; 689 BP.
DE Human prostate expression marker cDNA 12289.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 689;

Best Local Similarity 53.3%; Pred. No. 1.4e+02;
RESULT 1125
ID AAC54777 standard; DNA; 769 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 79053.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.0%; Score 30.8; DB 3; Length 769;
Best Local Similarity 48.3%; Pred. No. 1.5e+02;
RESULT 1126
ID AAC52294 standard; DNA; 771 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 70880.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.0%; Score 30.8; DB 3; Length 771;
Best Local Similarity 48.3%; Pred. No. 1.5e+02;
RESULT 1127
ID RAV06562 standard; cDNA; 2248 BP.
DE Arabidopsis cellulose synthase EST T20782 cDNA.
PN WO9800549-A1.
PD 08-JAN-1998.
PA (AUSU) UNIV AUSTRALIAN NAT.
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
Query Match 4.0%; Score 30.8; DB 2; Length 2248;
Best Local Similarity 54.4%; Pred. No. 2.5e+02;
RESULT 1128
ID ABK42634 standard; DNA; 3877 BP.
DE Genomic sequence #533 encoding novel human connective tissue polypeptide.
PN WO200155343-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 30.8; DB 4; Length 3877;
Best Local Similarity 51.4%; Pred. No. 3.2e+02;
RESULT 1129
ID ABA20095 standard; DNA; 3877 BP.
DE Human nervous system related polynucleotide SEQ ID NO 12426.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 30.8; DB 5; Length 3877;
Best Local Similarity 51.4%; Pred. No. 3.2e+02;
RESULT 1130
ID ADB60790 standard; DNA; 3877 BP.
DE Connective tissue related genomic DNA #533.
PN US2003054375-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 30.8; DB 9; Length 3877;
Best Local Similarity 51.4%; Pred. No. 3.2e+02;
RESULT 1131
ID ABK42632 standard; DNA; 3879 BP.
DE Genomic sequence #531 encoding novel human connective tissue polypeptide.
PN WO200155343-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 30.8; DB 4; Length 3879;
Best Local Similarity 51.4%; Pred. No. 3.2e+02;
RESULT 1132
ID ADB60788 standard; DNA; 3879 BP.
DE Connective tissue related genomic DNA #531.
PN US2003054375-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 30.8; DB 9; Length 3879;
Best Local Similarity 51.4%; Pred. No. 3.2e+02;
RESULT 1133
ID RAX55607 standard; DNA; 3960 BP.
DE Human clone 65 antisense sequence.
PN WO9921999-A2.
PD 06-MAY-1999.
PA (GETH) GENENTECH INC.
Query Match 4.0%; Score 30.8; DB 2; Length 3960;
Best Local Similarity 55.7%; Pred. No. 3.3e+02;
RESULT 1134

ID AAX55606 standard; DNA; 3960 BP.
DE Human clone 65 protein encoding DNA.
PN WO9921999-A2.
PD 06-MAY-1999.
PA (GETH) GENENTECH INC.
Query Match 4.0%; Score 30.8; DB 2; Length 3960;
Best Local Similarity 55.7%; Pred. No. 3.3e+02;
RESULT 1135
ID ACF64329 standard; DNA; 5148 BP.
DE Human ESR1 nucleotide sequence >ESR1_07.
PN WO2003014319-A2.
PD 20-FEB-2003.
PA (DNAS-) DNA SCI INC.
Query Match 4.0%; Score 30.8; DB 8; Length 5148;
Best Local Similarity 57.6%; Pred. No. 3.7e+02;
RESULT 1136
ID AAS61416 standard; DNA; 5887 BP.
DE Human gene regulation-associated gene oligonucleotide #371.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIC-) EPIGENOMICS AG.
Query Match 4.0%; Score 30.8; DB 6; Length 5887;
Best Local Similarity 55.7%; Pred. No. 3.9e+02;
RESULT 1137
ID AAD28372 standard; DNA; 6175 BP.
DE Human chemically treated genomic DNA #13.
PN WO200202809-A2.
PD 10-JAN-2002.
PA (EPIC-) EPIGENOMICS AG.
Query Match 4.0%; Score 30.8; DB 6; Length 6175;
Best Local Similarity 47.0%; Pred. No. 4e+02;
RESULT 1138
ID ADA69607 standard; DNA; 6477 BP.
DE Rice gene, SEQ ID 2930.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 4.0%; Score 30.8; DB 8; Length 6477;
Best Local Similarity 47.8%; Pred. No. 4.1e+02;
RESULT 1139
ID ABN80082 standard; DNA; 10250 BP.
DE Human chemically modified disease associated gene SEQ ID NO 99.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIC-) EPIGENOMICS AG.
Query Match 4.0%; Score 30.8; DB 6; Length 10250;
Best Local Similarity 48.8%; Pred. No. 5.1e+02;
RESULT 1140
ID ABL33544 standard; DNA; 10328 BP.
DE Human immune system associated gene SEQ ID NO: 1517.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIC-) EPIGENOMICS AG.
Query Match 4.0%; Score 30.8; DB 6; Length 10328;
Best Local Similarity 52.3%; Pred. No. 5.1e+02;
RESULT 1141
ID ABL32281 standard; DNA; 13511 BP.
DE Human immune system associated gene SEQ ID NO: 254.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIC-) EPIGENOMICS AG.
Query Match 4.0%; Score 30.8; DB 6; Length 13511;
Best Local Similarity 46.7%; Pred. No. 5.8e+02;
RESULT 1142
ID ABL05454 standard; cDNA; 13815 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 10844.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.0%; Score 30.8; DB 4; Length 13815;
Best Local Similarity 61.0%; Pred. No. 5.9e+02;
RESULT 1143
ID ABL70460 standard; DNA; 16228 BP.

DE Chemically treated cell signalling DNA sequence complementary to#175.
PN W0200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 30.8; DB 6; Length 16228;
Best Local Similarity 45.7%; Pred. No. 6.3e+02;
RESULT 1144
ID AAS61425 standard; DNA; 16228 BP.
DE Human gene regulation-associated gene oligonucleotide #380.
PN W0200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 30.8; DB 6; Length 16228;
Best Local Similarity 45.7%; Pred. No. 6.3e+02;
RESULT 1145
ID ADA02753 standard; DNA; 54355 BP.
DE Mouse Morf carcinoma associated gene, SEQ ID NO:1271.
PN W02003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 4.0%; Score 30.8; DB 9; Length 54355;
Best Local Similarity 54.4%; Pred. No. 1.1e+03;
RESULT 1146
ID ADB72491 standard; DNA; 54355 BP.
DE Mouse Morf gene.
PN W02003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 4.0%; Score 30.8; DB 10; Length 54355;
Best Local Similarity 54.4%; Pred. No. 1.1e+03;
RESULT 1147
ID ADC85233 standard; DNA; 54355 BP.
DE Mouse Morf genomic sequence.
PN W02003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 4.0%; Score 30.8; DB 10; Length 54355;
Best Local Similarity 54.4%; Pred. No. 1.1e+03;
RESULT 1148
ID ADM74348 standard; DNA; 54355 BP.
DE Murine carcinoma associated (CA) nucleic acid #10.
PN US2004072154-A1.
PD 15-APR-2004.
PA (MORR/) MORRIS D W.
PA (ENGEL/) ENGELHARD E K.
Query Match 4.0%; Score 30.8; DB 12; Length 54355;
Best Local Similarity 54.4%; Pred. No. 1.1e+03;
RESULT 1149
ID ABL12402 standard; CDNA; 90104 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 31688.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.0%; Score 30.8; DB 4; Length 90104;
Best Local Similarity 46.0%; Pred. No. 1.4e+03;
RESULT 1150
ID ADH51151 standard; DNA; 151830 BP.
DE Protein phosphatase 2A beta-gamma subunit PPP2R2C gene.
PN W02004001068-A2.
PD 31-DEC-2003.
PA (GEST) GENSET SA.
Query Match 4.0%; Score 30.8; DB 12; Length 151830;
Best Local Similarity 76.0%; Pred. No. 1.8e+03;
RESULT 1151
ID ADM78027 standard; DNA; 151830 BP.
DE Human PPF2R2C genomic DNA.
PN W02004000875-A2.
PD 31-DEC-2003.
PA (GEST) GENSET SA.
Query Match 4.0%; Score 30.8; DB 12; Length 151830;
Best Local Similarity 76.0%; Pred. No. 1.8e+03;
RESULT 1152
ID ADF51132 standard; DNA; 243428 BP.

DE Human P-Rex1 genomic DNA sequence.
PN W02003080664-A1.
PD 02-OCT-2003.
PA (BABR-) BABRAHAM INST.
Query Match 4.0%; Score 30.8; DB 12; Length 243428;
Best Local Similarity 57.1%; Pred. No. 2.1e+03;
RESULT 1153
ID AAC27654 standard; CDNA; 347 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 31729.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 4.0%; Score 30.6; DB 3; Length 347;
Best Local Similarity 52.1%; Pred. No. 1.2e+02;
RESULT 1154
ID AAF18350 standard; DNA; 428 BP.
DE Lung cancer associated polynucleotide sequence SEQ ID 369.
PN W0200055180-A2.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match 4.0%; Score 30.6; DB 3; Length 428;
Best Local Similarity 57.4%; Pred. No. 1.3e+02;
RESULT 1155
ID AAS83465 standard; CDNA; 433 BP.
DE DNA encoding novel human diagnostic protein #19269.
PN W0200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.0%; Score 30.6; DB 5; Length 433;
Best Local Similarity 52.8%; Pred. No. 1.3e+02;
RESULT 1156
ID AAH11396 standard; CDNA; 532 BP.
DE Human CDNA clone (3'-primer) SEQ ID NO:8231.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 4.0%; Score 30.6; DB 4; Length 532;
Best Local Similarity 48.9%; Pred. No. 1.5e+02;
RESULT 1157
ID AAS67705 standard; CDNA; 608 BP.
DE DNA encoding novel human diagnostic protein #3509.
PN W0200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.0%; Score 30.6; DB 5; Length 608;
Best Local Similarity 52.8%; Pred. No. 1.6e+02;
RESULT 1158
ID ABN61662 standard; CDNA; 618 BP.
DE Human cancer related polynucleotide SEQ ID NO 1629.
PN W0200214500-A2.
PD 21-FEB-2002.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 4.0%; Score 30.6; DB 6; Length 618;
Best Local Similarity 46.2%; Pred. No. 1.6e+02;
RESULT 1159
ID ABZ12834 standard; DNA; 678 BP.
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 639.
PN W0200216855-A2.
PD 28-FEB-2002.
PA (SVGN) SYNGENTA PARTICIPATIONS AG.
PA (SCRI) SCRIPPS RES INST.
Query Match 4.0%; Score 30.6; DB 6; Length 678;
Best Local Similarity 58.1%; Pred. No. 1.6e+02;
RESULT 1160
ID AAH31554 standard; CDNA; 688 BP.
DE Human olfactory receptor polynucleotide, SEQ ID NO: 127.
PN W0200127158-A2.
PD 19-APR-2001.
PA (DIGI-) DIGISCENTS.
PA (YEDA) YEDA RES & DEV CO LTD.
Query Match 4.0%; Score 30.6; DB 4; Length 688;

Best Local Similarity 50.0%; Pred. No. 1.7e+02;
RESULT 1161
ID AAS80716 standard; cDNA; 966 BP.
DE DNA encoding novel human diagnostic protein #16520.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.0%; Score 30.6; DB 5; Length 966;
Best Local Similarity 48.1%; Pred. No. 1.9e+02;
RESULT 1162
ID ADE55607 standard; DNA; 990 BP.
DE Rat gene AJ007632, SEQ ID NO 1426.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 4.0%; Score 30.6; DB 10; Length 990;
Best Local Similarity 48.1%; Pred. No. 2e+02;
RESULT 1163
ID ADE55605 standard; DNA; 990 BP.
DE Rat gene AJ007632, SEQ ID NO 1424.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 4.0%; Score 30.6; DB 10; Length 990;
Best Local Similarity 48.1%; Pred. No. 2e+02;
RESULT 1164
ID ADA71680 standard; DNA; 1167 BP.
DE Rice gene, SEQ ID 5004.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 4.0%; Score 30.6; DB 8; Length 1167;
Best Local Similarity 30.6%; Pred. No. 2.1e+02;
RESULT 1165
ID ASX72215 standard; cDNA; 1251 BP.
DE Human NOVX polynucleotide #46.
PN WO200281498-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 4.0%; Score 30.6; DB 8; Length 1251;
Best Local Similarity 53.8%; Pred. No. 2.2e+02;
RESULT 1166
ID ABZ11583 standard; cDNA; 1354 BP.
DE Human polynucleotide SEQ ID NO 465.
PN WO200270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match 4.0%; Score 30.6; DB 6; Length 1354;
Best Local Similarity 47.2%; Pred. No. 2.3e+02;
RESULT 1167
ID ADM44101 standard; cDNA; 1354 BP.
DE Novel human arginine-rich protein cDNA #465.
PN US2004053250-A1.
PD 18-MAR-2004.
PA (TANG/) TANG Y T.
PA (XUEA/) XUE A.
PA (DRMA/) DRMANAC R T.
Query Match 4.0%; Score 30.6; DB 12; Length 1354;
Best Local Similarity 47.2%; Pred. No. 2.3e+02;
RESULT 1168
ID ADK57600 standard; DNA; 1803 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #4983.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
PA (DOWC) DOW AGROSCIENCES LLC.
Query Match 4.0%; Score 30.6; DB 10; Length 1803;
Best Local Similarity 62.3%; Pred. No. 2.6e+02;
RESULT 1169
ID AAC45222 standard; DNA; 1812 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 45735.

PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.0%; Score 30.6; DB 3; Length 1812;
Best Local Similarity 56.4%; Pred. No. 2.6e+02;
RESULT 1170
ID AAC36973 standard; DNA; 1812 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 15728.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.0%; Score 30.6; DB 3; Length 1812;
Best Local Similarity 56.4%; Pred. No. 2.6e+02;
RESULT 1171
ID ABL52758 standard; DNA; 1854 BP.
DE Plant defence gene promoter region P1075.
PN WO200212483-A1.
PD 14-FEB-2002.
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
PA (QUEE-) STATE QUEENSLAND DEPT PRIMARY IND.
PA (UYOU) UNIV QUEENSLAND.
PA (SUGA-) BUREAU SUGAR EXPERIMENT STATIONS.
PA (GRAI-) GRAINS RES & DEV CORP.
Query Match 4.0%; Score 30.6; DB 6; Length 1854;
Best Local Similarity 48.1%; Pred. No. 2.6e+02;
RESULT 1172
ID ABV25351 standard; cDNA; 2206 BP.
DE Human prostate expression marker cDNA 25342.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.6; DB 5; Length 2206;
Best Local Similarity 68.9%; Pred. No. 2.9e+02;
RESULT 1173
ID ACA36675 standard; DNA; 2463 BP.
DE Prokaryotic essential gene #18332.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.0%; Score 30.6; DB 8; Length 2463;
Best Local Similarity 53.8%; Pred. No. 3e+02;
RESULT 1174
ID AA70144 standard; DNA; 2874 BP.
DE Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:277.
PN WO200025728-A2.
PD 11-MAY-2000.
PA (HOFF/) HOFFMAN S.
PA (CARU/) CARUCCI D.
PA (GARD/) GARDNER M.
PA (VENT/) VENTER J C.
Query Match 4.0%; Score 30.6; DB 3; Length 2874;
Best Local Similarity 48.1%; Pred. No. 3.2e+02;
RESULT 1175
ID AAH18524 standard; cDNA; 2881 BP.
DE Human cDNA sequence SEQ ID NO:18667.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 4.0%; Score 30.6; DB 4; Length 2881;
Best Local Similarity 48.9%; Pred. No. 3.2e+02;
RESULT 1176
ID AAQ29186 standard; cDNA; 2981 BP.
DE cDNA encoding Plasmodium SERA gene.
PN WO9216616-A1.
PD 01-OCT-1992.
PA (VIRO-) VIROGENETICS CORP.
Query Match 4.0%; Score 30.6; DB 2; Length 2981;
Best Local Similarity 48.1%; Pred. No. 3.3e+02;
RESULT 1177
ID AAQ67867 standard; DNA; 2981 BP.
DE p126.15 SERA cDNA insert.
PN WO9416716-A1.
PD 04-AUG-1994.
PA (VIRO-) VIROGENETICS CORP.
Query Match 4.0%; Score 30.6; DB 2; Length 2981;

Best Local Similarity 48.1%; Pred. No. 3.3e+02;
RESULT 1178
ID AAQ080907 standard; cDNA; 2981 BP.
DE Plasmodium falciparum SERA gene cDNA.
PN W09428930-A1.
PD 22-DEC-1994.
PA (VIRO-) VIROGENETICS CORP.
Query Match 4.0%; Score 30.6; DB 2; Length 2981;
Best Local Similarity 48.1%; Pred. No. 3.3e+02;
RESULT 1179
ID AAQ08451 standard; cDNA; 2981 BP.
DE Plasmodium falciparum SERA p126.15 encoding cDNA.
PN US5942235-A.
PD 24-AUG-1999.
PA (HEAL-) HEALTH RES INC.
Query Match 4.0%; Score 30.6; DB 2; Length 2981;
Best Local Similarity 48.1%; Pred. No. 3.3e+02;
RESULT 1180
ID ABK15041 standard; cDNA; 3107 BP.
DE Plasmodium cDNA encoding serine repeat antigen, SERA.
PN US6333406-B1.
PD 25-DEC-2001.
PA (INSE/) INSELBURG J W.
PA (BZIK/) BZIK D J.
PA (HORI/) HORII T.
PA (SUGI/) SUGIYAMA T.
Query Match 4.0%; Score 30.6; DB 6; Length 3107;
Best Local Similarity 48.1%; Pred. No. 3.4e+02;
RESULT 1181
ID ABL61065 standard; cDNA; 3851 BP.
DE Proline-enriched gamma-carboxyl glutamate-protein 194.05 encoding cDNA.
PN CN1311106-A.
PD 16-JAN-2002.
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
Query Match 4.0%; Score 30.6; DB 6; Length 3851;
Best Local Similarity 48.9%; Pred. No. 3.7e+02;
RESULT 1182
ID AAN81157 standard; DNA; 3975 BP.
DE Malaria-specific gene encoding 140kD antigen.
PN EP283882-A.
PD 28-SEP-1988.
PA (BEHW) BEHRINGWERKE AG.
Query Match 4.0%; Score 30.6; DB 1; Length 3975;
Best Local Similarity 48.1%; Pred. No. 3.8e+02;
RESULT 1183
ID AAQ22999 standard; DNA; 3975 BP.
DE SERP gene.
PN EP474891-A.
PD 18-MAR-1992.
PA (BEHW) BEHRINGWERKE AG.
Query Match 4.0%; Score 30.6; DB 2; Length 3975;
Best Local Similarity 48.1%; Pred. No. 3.8e+02;
RESULT 1184
ID AAQ23570 standard; DNA; 4944 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6390.
PN W02004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 4.0%; Score 30.6; DB 12; Length 4944;
Best Local Similarity 58.1%; Pred. No. 4.2e+02;
RESULT 1185
ID AAQ03568 standard; DNA; 6124 BP.
DE Sequence encoding the SERA protein of Plasmodium.
PN W09001549-A.
PD 22-FEB-1990.
PA (DART-) DARTMOUTH COLLEGE.
Query Match 4.0%; Score 30.6; DB 2; Length 6124;
Best Local Similarity 48.1%; Pred. No. 4.6e+02;
RESULT 1186
ID ABK15042 standard; DNA; 6124 BP.
DE Plasmodium gene for serine repeat antigen, SERA.
PN US6333406-B1.
PD 25-DEC-2001.
PA (DART-) DARTMOUTH COLLEGE.
Query Match 4.0%; Score 30.6; DB 2; Length 6124;
Best Local Similarity 48.1%; Pred. No. 4.6e+02;
RESULT 1187
ID AAT18767 standard; cDNA; 6578 BP.
DE RSV RNA-dependent RNA-polymerase L cDNA.
PN W09610400-A1.
PD 11-APR-1996.
PA (UABR-) UAB RES FOUND.
Query Match 4.0%; Score 30.6; DB 2; Length 6578;
Best Local Similarity 49.7%; Pred. No. 4.8e+02;
RESULT 1188
ID AAV48171 standard; cDNA; 6578 BP.
DE Respiratory syncytial virus RNA dependent RNA polymerase.
PN US5789229-A.
PD 04-AUG-1998.
PA (UABR-) UAB RES FOUND.
Query Match 4.0%; Score 30.6; DB 2; Length 6578;
Best Local Similarity 49.7%; Pred. No. 4.8e+02;
RESULT 1189
ID AA166080 standard; DNA; 7523 BP.
DE Listeria monocytogenes ClpC ATPase (mec) gene (GenBank: U40604).
PN W0200170929-A2.
PD 27-SEP-2001.
PA (ARCH-) ARCH DEV CORP.
Query Match 4.0%; Score 30.6; DB 4; Length 7523;
Best Local Similarity 53.8%; Pred. No. 5.1e+02;
RESULT 1190
ID ABL32077 standard; DNA; 7728 BP.
DE Human immune system associated gene SEQ ID NO: 50.
PN W0200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 30.6; DB 6; Length 7728;
Best Local Similarity 47.6%; Pred. No. 5.1e+02;
RESULT 1191
ID AAD28367 standard; DNA; 7728 BP.
DE Human chemically treated genomic DNA #8.
PN W0200202809-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 30.6; DB 6; Length 7728;
Best Local Similarity 47.6%; Pred. No. 5.1e+02;
RESULT 1192
ID ABL19348 standard; DNA; 8124 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 9517.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.0%; Score 30.6; DB 4; Length 8124;
Best Local Similarity 56.4%; Pred. No. 5.3e+02;
RESULT 1193
ID ABL33544 standard; DNA; 10328 BP.
DE Human immune system associated gene SEQ ID NO: 1517.
PN W0200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 30.6; DB 6; Length 10328;
Best Local Similarity 49.1%; Pred. No. 5.9e+02;
RESULT 1194
ID AAS45410 standard; DNA; 11036 BP.
DE Chemically pretreated genomic DNA associated with cell cycle #58.
PN W0200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 30.6; DB 4; Length 11036;
Best Local Similarity 68.9%; Pred. No. 6.1e+02;
RESULT 1195
ID ABK28263 standard; DNA; 11036 BP.
DE DNA transcription associated genomic DNA #69.

PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 30.6; DB 6; Length 11036;
Best Local Similarity 68.9%; Pred. No. 6.1e+02;
RESULT 1196
ID AAL36231 standard; DNA; 13819 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 2596.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 30.6; DB 4; Length 13819;
Best Local Similarity 65.2%; Pred. No. 6.8e+02;
RESULT 1197
ID ABX59219 standard; cDNA; 13819 BP.
DE cDNA encoding novel human musculoskeletal system antigen #1563.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 4.0%; Score 30.6; DB 8; Length 13819;
Best Local Similarity 65.2%; Pred. No. 6.8e+02;
RESULT 1198
ID ADJ29969 standard; DNA; 13819 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 2596.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 30.6; DB 12; Length 13819;
Best Local Similarity 65.2%; Pred. No. 6.8e+02;
RESULT 1199
ID AAL36230 standard; DNA; 13821 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 2595.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 30.6; DB 4; Length 13821;
Best Local Similarity 65.2%; Pred. No. 6.8e+02;
RESULT 1200
ID ABX59218 standard; cDNA; 13821 BP.
DE cDNA encoding novel human musculoskeletal system antigen #1562.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 4.0%; Score 30.6; DB 8; Length 13821;
Best Local Similarity 65.2%; Pred. No. 6.8e+02;
RESULT 1201
ID ADJ29968 standard; DNA; 13821 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 2595.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 30.6; DB 12; Length 13821;
Best Local Similarity 65.2%; Pred. No. 6.8e+02;
RESULT 1202
ID AAX59703 standard; DNA; 15210 BP.
DE Polynucleotide sequence of RSV strain A2.
PN WO9922742-A1.
PD 14-MAY-1999.
PA (CLEV-) CLEVELAND CLINIC FOUND.
PA (USSH) US NAT INST OF HEALTH.
Query Match 4.0%; Score 30.6; DB 2; Length 15210;
Best Local Similarity 49.7%; Pred. No. 7.1e+02;
RESULT 1203
ID AAT78440 standard; DNA; 15222 BP.
DE Human respiratory syncytial virus strain A2.
PN WO9729757-A1.
PD 21-AUG-1997.
PA (CLEV-) CLEVELAND CLINIC FOUND.
PA (USSH) US NAT INST OF HEALTH.

Query Match 4.0%; Score 30.6; DB 2; Length 15222;
Best Local Similarity 49.7%; Pred. No. 7.1e+02;
RESULT 1204
ID AAT63430 standard; DNA; 15223 BP.
DE Respiratory syncytial virus anti-genome.
PN WO9712032-A1.
PD 03-APR-1997.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 4.0%; Score 30.6; DB 2; Length 15223;
Best Local Similarity 49.7%; Pred. No. 7.1e+02;
RESULT 1205
ID AAV17553 standard; cDNA; 15223 BP.
DE Respiratory syncytial virus antigenome.
PN WO9802530-A1.
PD 22-JAN-1998.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 4.0%; Score 30.6; DB 2; Length 15223;
Best Local Similarity 49.7%; Pred. No. 7.1e+02;
RESULT 1206
ID AAA88743 standard; cDNA; 15223 BP.
DE Respiratory syncytial virus D46 5'-3' positive sense sequence.
PN WO200061611-A2.
PD 19-OCT-2000.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 4.0%; Score 30.6; DB 3; Length 15223;
Best Local Similarity 49.7%; Pred. No. 7.1e+02;
RESULT 1207
ID ABL32050 standard; DNA; 16545 BP.
DE Human immune system associated gene SEQ ID NO: 23.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 30.6; DB 6; Length 16545;
Best Local Similarity 55.0%; Pred. No. 7.4e+02;
RESULT 1208
ID ABK31171 standard; DNA; 17293 BP.
DE Signal transduction associated gene modified complementary DNA #7.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 30.6; DB 6; Length 17293;
Best Local Similarity 49.1%; Pred. No. 7.5e+02;
RESULT 1209
ID ABL70126 standard; DNA; 17293 BP.
DE Chemically treated cell signalling DNA sequence complementary to#8.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 30.6; DB 6; Length 17293;
Best Local Similarity 49.1%; Pred. No. 7.5e+02;
RESULT 1210
ID AAS61058 standard; DNA; 17293 BP.
DE Human gene regulation-associated gene oligonucleotide #13.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 30.6; DB 6; Length 17293;
Best Local Similarity 49.1%; Pred. No. 7.5e+02;
RESULT 1211
ID AAK71667 standard; DNA; 17379 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:26479.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 30.6; DB 4; Length 17379;
Best Local Similarity 55.0%; Pred. No. 7.5e+02;
RESULT 1212
ID AAS28427 standard; DNA; 17379 BP.
DE Genomic sequence #267 encoding for novel human respiratory antigen.
PN WO200155448-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 30.6; DB 4; Length 17379;

Best Local Similarity 55.0%; Pred. No. 7.5e+02;
RESULT 1213
ID ADG41623 standard; DNA; 17379 BP.
DE Human respiratory system associated genomic DNA seq id 861.
PN US2003215893-A1.
PD 20-NOV-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 30.6; DB 10; Length 17379;
Best Local Similarity 55.0%; Pred. No. 7.5e+02;
RESULT 1214
ID ABL16042 standard; cDNA; 22253 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 42608.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.0%; Score 30.6; DB 4; Length 22253;
Best Local Similarity 48.6%; Pred. No. 8.4e+02;
RESULT 1215
ID ADC20666 standard; DNA; 51961 BP.
DE Human secreted protein-related DNA sequence #84.
PN WO200292787-A2.
PD 21-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 30.6; DB 10; Length 51961;
Best Local Similarity 52.8%; Pred. No. 1.2e+03;
RESULT 1216
ID APT16905 standard; DNA; 51961 BP.
DE Human secreted protein-related DNA sequence - SEQ ID NO 259.
PN WO200277188-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 30.6; DB 10; Length 51961;
Best Local Similarity 52.8%; Pred. No. 1.2e+03;
RESULT 1217
ID ASZ67488 standard; DNA; 51961 BP.
DE Human secreted protein encoding genomic DNA SEQ ID NO 1011.
PN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 30.6; DB 10; Length 51961;
Best Local Similarity 52.8%; Pred. No. 1.2e+03;
RESULT 1218
ID AAF22303 standard; DNA; 611590 BP.
DE Arabidopsis thaliana chromosome 2 centromere.
PN WO200055325-A2.
PD 21-SEP-2000.
PA (UYCH-) UNIV CHICAGO.
Query Match 4.0%; Score 30.6; DB 3; Length 110000;
Best Local Similarity 51.1%; Pred. No. 1.8e+03;
RESULT 1220
ID AAD54634 standard; DNA; 142519 BP.
DE Human chromodomain helicase DNA binding protein (CHD) encoding DNA #9.
PN WO200298899-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 4.0%; Score 30.6; DB 10; Length 142519;
Best Local Similarity 46.2%; Pred. No. 2e+03;
RESULT 1223
ID ADH30232 standard; DNA; 161671 BP.
DE Human PLOD2 DNA.
PN US2003124535-A1.
PD 03-JUL-2003.
PA (VITI-) VITIVITY INC.
Query Match 4.0%; Score 30.6; DB 12; Length 161671;

Best Local Similarity 46.2%; Pred. No. 2.1e+03;
RESULT 1224
ID ABS5200 standard; DNA; 341511 BP.
DE Genomic DNA encoding human transporter protein.
Query Match 4.0%; Score 30.6; DB 6; Length 341511;
Best Local Similarity 50.3%; Pred. No. 2.7e+03;
RESULT 1225
ID ADO05495 standard; DNA; 280 BP.
DE Soybean zinc finger transcription factor seqid 2341.
PN US2004123339-A1.
PD 24-JUN-2004.
PA (CONV/) CONNER T W.
PA (HECK/) HECK G R.
PA (LIUJ/) LIU J.
Query Match 4.0%; Score 30.4; DB 12; Length 280;
Best Local Similarity 53.3%; Pred. No. 1.3e+02;
RESULT 1226
ID ABL62993 standard; DNA; 308 BP.
DE Breast cancer related gene sequence SEQ ID NO:1330.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 4.0%; Score 30.4; DB 6; Length 308;
Best Local Similarity 45.4%; Pred. No. 1.3e+02;
RESULT 1227
ID ABL62809 standard; DNA; 308 BP.
DE Breast cancer related gene sequence SEQ ID NO:1146.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 4.0%; Score 30.4; DB 6; Length 308;
Best Local Similarity 45.4%; Pred. No. 1.3e+02;
RESULT 1228
ID ABL62070 standard; DNA; 308 BP.
DE Colon adenocarcinoma related gene sequence SEQ ID NO:407.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 4.0%; Score 30.4; DB 6; Length 308;
Best Local Similarity 45.4%; Pred. No. 1.3e+02;
RESULT 1229
ID ABV02543 standard; cDNA; 438 BP.
DE Human prostate expression marker cDNA 2534.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.4; DB 5; Length 438;
Best Local Similarity 52.5%; Pred. No. 1.5e+02;
RESULT 1230
ID ACH72411 standard; DNA; 600 BP.
DE Human genome derived single exon probe #5606.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 4.0%; Score 30.4; DB 12; Length 600;
Best Local Similarity 55.8%; Pred. No. 1.8e+02;
RESULT 1231
ID ABV51715 standard; cDNA; 606 BP.
DE Human prostate expression marker cDNA 51706.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.4; DB 5; Length 606;
Best Local Similarity 63.9%; Pred. No. 1.8e+02;
RESULT 1232
ID ABN62149 standard; cDNA; 618 BP.
DE Human cancer related polynucleotide SEQ ID NO 2116.
PN WO200214500-A2.
PD 21-FEB-2002.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.

Query Match 4.0%; Score 30.4; DB 6; Length 618;
Best Local Similarity 53.3%; Pred. No. 1.8e+02;
RESULT 1233
ID AA195397 standard; cDNA; 756 BP.
DE Human neuroblastoma expressed polynucleotide SEQ ID NO 1472.
PN WO200166719-A1.
PD 13-SEP-2001.
PA (CHIB-) CHIBA PREFECTURE.
PA (HISM) HISAMITSU PHARM CO LTD.
Query Match 4.0%; Score 30.4; DB 4; Length 756;
Best Local Similarity 63.2%; Pred. No. 2e+02;
RESULT 1234
ID AA195724 standard; cDNA; 783 BP.
DE Human neuroblastoma expressed polynucleotide SEQ ID NO 1799.
PN WO200166719-A1.
PD 13-SEP-2001.
PA (CHIB-) CHIBA PREFECTURE.
PA (HISM) HISAMITSU PHARM CO LTD.
Query Match 4.0%; Score 30.4; DB 4; Length 783;
Best Local Similarity 48.8%; Pred. No. 2e+02;
RESULT 1235
ID AAH08126 standard; cDNA; 792 BP.
DE Human cDNA clone (5'-primer) SEQ ID NO:4961.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 4.0%; Score 30.4; DB 4; Length 792;
Best Local Similarity 63.9%; Pred. No. 2e+02;
RESULT 1236
ID ADO62586 standard; DNA; 823 BP.
DE Transcription factor G1779 orthologous sequence, SEQ ID 1053.
PN WO2004031349-A2.
PD 15-APR-2004.
PA (MEN-) MENDEL BIOTECHNOLOGY INC.
Query Match 4.0%; Score 30.4; DB 12; Length 823;
Best Local Similarity 53.3%; Pred. No. 2.1e+02;
RESULT 1237
ID AAS71828 standard; cDNA; 981 BP.
DE DNA encoding novel human diagnostic protein #7632.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.0%; Score 30.4; DB 5; Length 981;
Best Local Similarity 54.5%; Pred. No. 2.3e+02;
RESULT 1238
ID ACF72474 standard; DNA; 1062 BP.
DE Staphylococcus aureus DNA #154.
PN WO200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match 4.0%; Score 30.4; DB 8; Length 1062;
Best Local Similarity 50.0%; Pred. No. 2.3e+02;
RESULT 1239
ID AAS55149 standard; DNA; 1065 BP.
DE Staphylococcus aureus DNA for cellular proliferation protein #1461.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.0%; Score 30.4; DB 4; Length 1065;
Best Local Similarity 50.0%; Pred. No. 2.3e+02;
RESULT 1240
ID AAX83358 standard; cDNA; 1205 BP.
DE Breast cancer tumour specific clone #112.
PN WO9725426-A2.
PD 17-JUL-1997.
PA (CORI-) CORIXA CORP.
Query Match 4.0%; Score 30.4; DB 2; Length 1205;
Best Local Similarity 45.4%; Pred. No. 2.5e+02;
RESULT 1241
ID AAC08081 standard; cDNA; 1205 BP.
DE Human breast tumour-specific cDNA SEQ ID NO: 169.
PN WO200061753-A2.
PD 19-OCT-2000.

PA (CORI-) CORIXA CORP.
Query Match 4.0%; Score 30.4; DB 3; Length 1205;
Best Local Similarity 45.4%; Pred. No. 2.5e+02;
RESULT 1242
ID AAS99727 standard; cDNA; 1205 BP.
DE Breast tumour-specific DNA #102.
PN WO200190152-A2.
PD 29-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 4.0%; Score 30.4; DB 6; Length 1205;
Best Local Similarity 45.4%; Pred. No. 2.5e+02;
RESULT 1243
ID ABK46771 standard; cDNA; 1205 BP.
DE Human breast tumour-specific cDNA #89.
PN US6344550-B1.
PD 05-FEB-2002.
PA (CORI-) CORIXA CORP.
Query Match 4.0%; Score 30.4; DB 6; Length 1205;
Best Local Similarity 45.4%; Pred. No. 2.5e+02;
RESULT 1244
ID AAK72633 standard; DNA; 1223 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27445.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 30.4; DB 4; Length 1223;
Best Local Similarity 53.3%; Pred. No. 2.5e+02;
RESULT 1245
ID AAK72634 standard; DNA; 1224 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27446.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 30.4; DB 4; Length 1224;
Best Local Similarity 53.3%; Pred. No. 2.5e+02;
RESULT 1246
ID AAV68898 standard; DNA; 1265 BP.
DE DNA molecule encoding a breast tumour specific polypeptide #90.
PN WO9845328-A2.
PD 15-OCT-1998.
PA (CORI-) CORIXA CORP.
Query Match 4.0%; Score 30.4; DB 2; Length 1265;
Best Local Similarity 45.4%; Pred. No. 2.5e+02;
RESULT 1247
ID ADA11248 standard; cDNA; 1265 BP.
DE Human breast cancer specific cDNA #104.
PN US2002165371-A1.
PD 07-NOV-2002.
PA (FRUD/) FRUDAKIS T N.
PA (REED/) REED S G.
PA (SMIT/) SMITH J M.
PA (MISH/) MISHNER L E.
PA (DILL/) DILLON D C.
PA (RETT/) RETTER M W.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HARL/) HARLOCKER S L.
PA (DAYC/) DAY C H.
PA (LISX/) LI S X.
PA (DENG/) DENG T.
Query Match 4.0%; Score 30.4; DB 8; Length 1265;
Best Local Similarity 45.4%; Pred. No. 2.5e+02;
RESULT 1248
ID ADC15221 standard; cDNA; 1265 BP.
DE Human breast tumour protein cDNA, SEQ ID 169.
PN WO2003013431-A2.
PD 20-FEB-2003.
PA (CORI-) CORIXA CORP.
Query Match 4.0%; Score 30.4; DB 10; Length 1265;
Best Local Similarity 45.4%; Pred. No. 2.5e+02;
RESULT 1249
ID ADM01599 standard; cDNA; 2118 BP.
DE Human cDNA of the invention SEQ ID NO:284.

PN EPI347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 4.0%; Score 30.4; DB 11; Length 2118;
Best Local Similarity 53.3%; Pred. No. 3.2e+02;
RESULT 1250
ID RAC99030 standard; cDNA; 2217 BP.
DE Human pancreatic cancer antigen nucleotide sequence SEQ ID NO:258.
PN WO200055320-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 30.4; DB 3; Length 2217;
Best Local Similarity 45.4%; Pred. No. 3.3e+02;
RESULT 1251
ID ACC72667 standard; cDNA; 2373 BP.
DE Human cancer related protein encoding cDNA SEQ ID NO:6.
PN WO2003025138-A2.
PD 27-MAR-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 4.0%; Score 30.4; DB 10; Length 2373;
Best Local Similarity 45.4%; Pred. No. 3.4e+02;
RESULT 1252
ID ADO25329 standard; DNA; 2373 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 8149.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 4.0%; Score 30.4; DB 12; Length 2373;
Best Local Similarity 45.4%; Pred. No. 3.4e+02;
RESULT 1253
ID AAH72845 standard; cDNA; 2950 BP.
DE Human cervical cancer marker nucleic acid 4119.
PN WO200142467-A2.
PD 14-JUN-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.4; DB 4; Length 2950;
Best Local Similarity 45.4%; Pred. No. 3.8e+02;
RESULT 1254
ID AAH72686 standard; cDNA; 2950 BP.
DE Human cervical cancer marker nucleic acid 3960.
PN WO200142467-A2.
PD 14-JUN-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.4; DB 4; Length 2950;
Best Local Similarity 45.4%; Pred. No. 3.8e+02;
RESULT 1255
ID ADL46049 standard; DNA; 2987 BP.
DE Human ovarian cancer DNA marker #19939.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.4; DB 5; Length 2987;
Best Local Similarity 45.4%; Pred. No. 3.8e+02;
RESULT 1256
ID ADI05016 standard; DNA; 3204 BP.
DE aadA/BADH expression cassette.
PN WO2004005480-A2.
PD 15-JAN-2004.
PA (UYFL-) UNIV CENT FLORIDA.
Query Match 4.0%; Score 30.4; DB 12; Length 3204;
Best Local Similarity 53.3%; Pred. No. 3.9e+02;
RESULT 1257
ID ADI05017 standard; DNA; 3300 BP.
DE gfp/BADH expression cassette.
PN WO2004005480-A2.
PD 15-JAN-2004.
PA (UYFL-) UNIV CENT FLORIDA.
Query Match 4.0%; Score 30.4; DB 12; Length 3300;
Best Local Similarity 53.3%; Pred. No. 4e+02;
RESULT 1258
ID AAH70099 standard; DNA; 3579 BP.
DE Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:232.
PN WO200025728-A2.

PD 11-MAY-2000.
PA (HOPE/) HOFFMAN S.
PA (CARU/) CARUCCI D.
PA (GARD/) GARDNER M.
PA (VENT/) VENTER J C.
Query Match 4.0%; Score 30.4; DB 3; Length 3579;
Best Local Similarity 55.8%; Pred. No. 4.1e+02;
RESULT 1259
ID ABT17682 standard; DNA; 4208 BP.
DE Aspergillus fumigatus essential gene #40.
PN WO200286090-A2.
PD 31-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.0%; Score 30.4; DB 8; Length 4208;
Best Local Similarity 61.2%; Pred. No. 4.5e+02;
RESULT 1260
ID ABT19496 standard; DNA; 4529 BP.
DE Aspergillus fumigatus essential gene #1854.
PN WO200286090-A2.
PD 31-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.0%; Score 30.4; DB 8; Length 4529;
Best Local Similarity 61.2%; Pred. No. 4.6e+02;
RESULT 1261
ID AAS71832 standard; cDNA; 4651 BP.
DE DNA encoding novel human diagnostic protein #7636.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSB-) HYSB INC.
Query Match 4.0%; Score 30.4; DB 5; Length 4651;
Best Local Similarity 54.5%; Pred. No. 4.7e+02;
RESULT 1262
ID ABL30444 standard; DNA; 5223 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 42805.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.0%; Score 30.4; DB 4; Length 5223;
Best Local Similarity 47.0%; Pred. No. 4.9e+02;
RESULT 1263
ID ABK33934 standard; DNA; 5310 BP.
DE Human DNA for staging of Astrocytomas #9.
PN WO200202808-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 30.4; DB 6; Length 5310;
Best Local Similarity 48.8%; Pred. No. 5e+02;
RESULT 1264
ID ADA20346 standard; DNA; 5310 BP.
DE Prostate tumour related genomic DNA sample #6.
PN WO2002103042-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 30.4; DB 8; Length 5310;
Best Local Similarity 48.8%; Pred. No. 5e+02;
RESULT 1265
ID ADA84153 standard; DNA; 5310 BP.
DE Human renal/prostate carcinoma associated DNA SEQ ID NO:11.
PN WO2002103041-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 30.4; DB 8; Length 5310;
Best Local Similarity 48.8%; Pred. No. 5e+02;
RESULT 1266
ID ADE84083 standard; DNA; 5310 BP.
DE Human lymphoid cell proliferative disorder gene derived DNA #19.
PN WO2003044226-A2.
PD 30-MAY-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 30.4; DB 10; Length 5310;
Best Local Similarity 48.8%; Pred. No. 5e+02;
RESULT 1267
ID ABL32132 standard; DNA; 5421 BP.

DE Human immune system associated gene SEQ ID NO: 105.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 30.4; DB 6; Length 5421;
Best Local Similarity 71.4%; Pred. No. 5e+02;
RESULT 1268
ID AAV74613 standard; DNA; 7159 BP.
DE Staphylococcus aureus contig SEQ ID #302.
PN EP786519-A2.
PD 30-JUL-1997.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 30.4; DB 2; Length 7159;
Best Local Similarity 50.0%; Pred. No. 5.7e+02;
RESULT 1269
ID ABL32896 standard; DNA; 8131 BP.
DE Human immune system associated gene SEQ ID NO: 869.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 30.4; DB 6; Length 8131;
Best Local Similarity 55.8%; Pred. No. 6.1e+02;
RESULT 1270
ID AAS63326 standard; DNA; 8131 BP.
DE Chemically pretreated metabolism associated gene #21.
PN WO200176451-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 30.4; DB 6; Length 8131;
Best Local Similarity 55.8%; Pred. No. 6.1e+02;
RESULT 1271
ID ABL31277 standard; DNA; 9087 BP.
DE Signal transduction associated gene modified complementary DNA #60.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 30.4; DB 6; Length 9087;
Best Local Similarity 49.4%; Pred. No. 6.4e+02;
RESULT 1272
ID ABL70238 standard; DNA; 9087 BP.
DE Chemically treated cell signalling DNA sequence complementary to #64.
PN WO200200928-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 30.4; DB 6; Length 9087;
Best Local Similarity 49.4%; Pred. No. 6.4e+02;
RESULT 1273
ID AAS61181 standard; DNA; 9087 BP.
DE Human gene regulation-associated gene oligonucleotide #136.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 30.4; DB 6; Length 9087;
Best Local Similarity 49.4%; Pred. No. 6.4e+02;
RESULT 1274
ID ABL04304 standard; cDNA; 13359 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 7394.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.0%; Score 30.4; DB 4; Length 13359;
Best Local Similarity 47.4%; Pred. No. 7.6e+02;
RESULT 1275
ID ABL32466 standard; DNA; 15373 BP.
DE Human immune system associated gene SEQ ID NO: 439.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 30.4; DB 6; Length 15373;
Best Local Similarity 47.4%; Pred. No. 8.2e+02;
RESULT 1276
ID ABL32185 standard; DNA; 15387 BP.
DE Human immune system associated gene SEQ ID NO: 158.

PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 30.4; DB 6; Length 15387;
Best Local Similarity 55.8%; Pred. No. 8.2e+02;
RESULT 1277
ID ABL33207 standard; DNA; 15767 BP.
DE Human immune system associated gene SEQ ID NO: 1180.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 30.4; DB 6; Length 15767;
Best Local Similarity 49.4%; Pred. No. 8.3e+02;
RESULT 1278
ID ABL34553 standard; DNA; 15767 BP.
DE Human metastasis associated gene SEQ ID NO: 106.
PN WO200177376-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 30.4; DB 6; Length 15767;
Best Local Similarity 49.4%; Pred. No. 8.3e+02;
RESULT 1279
ID ABL30408 standard; DNA; 15933 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 42697.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.0%; Score 30.4; DB 4; Length 15933;
Best Local Similarity 47.0%; Pred. No. 8.3e+02;
RESULT 1280
ID AAK73082 standard; DNA; 20188 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO: 27894.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 30.4; DB 4; Length 20188;
Best Local Similarity 55.8%; Pred. No. 9.3e+02;
RESULT 1281
ID AAK87550 standard; DNA; 20188 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO: 42362.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 30.4; DB 4; Length 20188;
Best Local Similarity 55.8%; Pred. No. 9.3e+02;
RESULT 1282
ID ABA07406 standard; DNA; 32249 BP.
DE Human pancreatic cancer related genomic DNA, SEQ ID NO: 725.
PN WO200155206-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 30.4; DB 4; Length 32249;
Best Local Similarity 55.8%; Pred. No. 1.2e+03;
RESULT 1283
ID AAK91137 standard; DNA; 32249 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 4713.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 30.4; DB 4; Length 32249;
Best Local Similarity 55.8%; Pred. No. 1.2e+03;
RESULT 1284
ID ABA20005 standard; DNA; 32249 BP.
DE Human nervous system related polynucleotide SEQ ID NO 12336.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 30.4; DB 5; Length 32249;
Best Local Similarity 55.8%; Pred. No. 1.2e+03;
RESULT 1285
ID AAK87551 standard; DNA; 50442 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO: 42363.
PN WO200157182-A2.

PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 30.4; DB 4; Length 50442;
Best Local Similarity 55.8%; Pred. No. 1.4e+03;
RESULT 1286
ID AAK73083 standard; DNA; 50442 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27895.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 30.4; DB 4; Length 50442;
Best Local Similarity 55.8%; Pred. No. 1.4e+03;
RESULT 1287
ID ADA02798 standard; DNA; 52754 BP.
DE Human TNFSF11 carcinoma associated gene, SEQ ID NO:1316.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 4.0%; Score 30.4; DB 9; Length 52754;
Best Local Similarity 46.0%; Pred. No. 1.4e+03;
RESULT 1288
ID ADB72536 standard; DNA; 52754 BP.
DE Human TNFSF11 gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 4.0%; Score 30.4; DB 10; Length 52754;
Best Local Similarity 46.0%; Pred. No. 1.4e+03;
RESULT 1289
ID ADC85278 standard; DNA; 52754 BP.
DE Human TNfsf11 genomic sequence.
PN WO2003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 4.0%; Score 30.4; DB 10; Length 52754;
Best Local Similarity 46.0%; Pred. No. 1.4e+03;
RESULT 1290
ID ADM74393 standard; DNA; 52754 BP.
DE Human carcinoma associated (CA) nucleic acid #31.
PN US2004072154-A1.
PD 15-APR-2004.
PA (MORR/) MORRIS D W.
PA (ENGE/) ENGELHARD E K.
Query Match 4.0%; Score 30.4; DB 12; Length 52754;
Best Local Similarity 46.0%; Pred. No. 1.4e+03;
RESULT 1291
Query Match 4.0%; Score 30.4; DB 2; Length 110000;
Best Local Similarity 45.2%; Pred. No. 2e+03;
RESULT 1292
ID ADF77343 standard; DNA; 1983043 BP.
DE Lactic acid bacteria Lactobacillus johnsonii Lal genomic DNA SEQ ID NO:1.
PN WO2003084989-A2.
PD 16-OCT-2003.
PA (NEST) SOC PROD NESTLE SA.
Query Match 4.0%; Score 30.4; DB 10; Length 110000;
Best Local Similarity 50.7%; Pred. No. 2e+03;
RESULT 1293
ID ADF13110 standard; DNA; 118067 BP.
DE Hypermethylation site in human breast cancer CpG island locus HBC-37.
PN US2003123602-A1.
PD 10-JUL-2003.
PA (HUAN/) HUANG T H.
Query Match 4.0%; Score 30.4; DB 12; Length 118067;
Best Local Similarity 47.4%; Pred. No. 2.1e+03;
RESULT 1294
ID ADI37256 standard; DNA; 118067 BP.
DE Hypermethylation in cancer (HBC) locus-37.
PN US605432-B1.
PD 12-AUG-2003.
PA (UMOR) UNIV MISSOURI.
Query Match 4.0%; Score 30.4; DB 12; Length 118067;
Best Local Similarity 47.4%; Pred. No. 2.1e+03;
RESULT 1295

ID ADL08126 standard; DNA; 191395 BP.
DE Human gene associated with low HDL-C PAI2.
PN US2004043389-A1.
PD 04-MAR-2004.
PA (VITI-) VITIVITY INC.
Query Match 4.0%; Score 30.4; DB 12; Length 191395;
Best Local Similarity 50.0%; Pred. No. 2.5e+03;
RESULT 1296
ID AAC06534 standard; cDNA; 442 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 10609.
PN EPI033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 3.9%; Score 30.2; DB 3; Length 442;
Best Local Similarity 50.4%; Pred. No. 1.8e+02;
RESULT 1297
ID ABV52363 standard; cDNA; 493 BP.
DE Human prostate expression marker cDNA 52354.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.9%; Score 30.2; DB 5; Length 493;
Best Local Similarity 56.6%; Pred. No. 1.9e+02;
RESULT 1298
ID ADQ18344 standard; DNA; 532 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1163.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 3.9%; Score 30.2; DB 12; Length 532;
Best Local Similarity 52.8%; Pred. No. 1.9e+02;
RESULT 1299
ID AAF68671 standard; cDNA; 572 BP.
DE Human lung tumour protein related nucleotide sequence SEQ ID NO:606.
PN WO200100828-A2.
PD 04-JAN-2001.
PA (CORI-) CORIXA CORP.
Query Match 3.9%; Score 30.2; DB 5; Length 572;
Best Local Similarity 47.9%; Pred. No. 2e+02;
RESULT 1300
ID ABK38582 standard; cDNA; 572 BP.
DE cDNA encoding clone #26264 of lung tumour protein.
PN WO200204514-A2.
PD 17-JAN-2002.
PA (CORI-) CORIXA CORP.
Query Match 3.9%; Score 30.2; DB 6; Length 572;
Best Local Similarity 47.9%; Pred. No. 2e+02;
RESULT 1301
ID ACA10911 standard; cDNA; 572 BP.
DE Human lung neuroendocrine carcinoma library MLN1 cDNA, SEQ ID 606.
PN US2002197669-A1.
PD 26-DEC-2002.
PA (BANG/) BANGUR C S.
PA (FANG/) FANGER G R.
PA (WANG/) WANG A.
PA (WANG/) WANG T.
PA (SWIT/) SWITZER A P.
PA (MCNE/) MCNEILL P D.
PA (CLAP/) CLAPPER J D.
Query Match 3.9%; Score 30.2; DB 8; Length 572;
Best Local Similarity 47.9%; Pred. No. 2e+02;
RESULT 1302
ID ABX99862 standard; cDNA; 572 BP.
DE Lung cancer therapy and diagnosis associated cDNA #589.
PN US2002172952-A1.
PD 21-NOV-2002.
PA (CORI-) CORIXA CORP.
Query Match 3.9%; Score 30.2; DB 8; Length 572;
Best Local Similarity 47.9%; Pred. No. 2e+02;
RESULT 1303
ID ADH46125 standard; cDNA; 572 BP.
DE Human lung tumour cDNA clone, SEQ ID NO 606.
PN WO2003037267-A2.

PD 08-MAY-2003.
 PA (CORI-) CORIXA CORP.
 Query Match 3.9%; Score 30.2; DB 10; Length 572;
 Best Local Similarity 47.9%; Pred. No. 2e+02;
 RESULT 1304
 ID ADE71877 standard; cDNA; 572 BP.
 DE Human lung tumour protein cDNA #589.
 PN US2003125245-A1.
 PD 03-JUL-2003.
 PA (WANG/) WANG T.
 PA (BANG/) BANGUR C S.
 Query Match 3.9%; Score 30.2; DB 12; Length 572;
 Best Local Similarity 47.9%; Pred. No. 2e+02;
 RESULT 1305
 ID ABL90425 standard; cDNA; 637 BP.
 DE Human polynucleotide SEQ ID NO 987.
 PN WO200190304-A2.
 PD 29-NOV-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 3.9%; Score 30.2; DB 6; Length 637;
 Best Local Similarity 56.0%; Pred. No. 2.1e+02;
 RESULT 1306
 ID AAG55740 standard; DNA; 895 BP.
 DE Streptococcus pneumoniae DNA for cellular proliferation protein #311.
 PN WO200170955-A2.
 PD 27-SEP-2001.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 3.9%; Score 30.2; DB 4; Length 885;
 Best Local Similarity 53.9%; Pred. No. 2.5e+02;
 RESULT 1307
 ID ACA50066 standard; DNA; 885 BP.
 DE Prokaryotic essential gene #31723.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 3.9%; Score 30.2; DB 8; Length 885;
 Best Local Similarity 53.9%; Pred. No. 2.5e+02;
 RESULT 1308
 ID ADC85778 standard; DNA; 985 BP.
 DE Human GPCR gene SEQ ID NO:231.
 PN EP1270724-A2.
 PD 02-JAN-2003.
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
 Query Match 3.9%; Score 30.2; DB 10; Length 985;
 Best Local Similarity 58.2%; Pred. No. 2.6e+02;
 RESULT 1309
 ID ADA30374 standard; DNA; 1014 BP.
 DE DNA encoding Acinetobacter baumannii protein #1661.
 PN US652958-B1.
 PD 13-MAY-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 3.9%; Score 30.2; DB 9; Length 1014;
 Best Local Similarity 56.6%; Pred. No. 2.6e+02;
 RESULT 1310
 ID ABQ76477 standard; cDNA; 1235 BP.
 DE S. cerevisiae BAX-associated cDNA fragment SEQ ID 379.
 PN WO00264766-A2.
 PD 22-AUG-2002.
 PA (JANC-) JANSSEN PHARM NV.
 Query Match 3.9%; Score 30.2; DB 6; Length 1235;
 Best Local Similarity 53.9%; Pred. No. 2.9e+02;
 RESULT 1311
 ID ADP41695 standard; DNA; 1353 BP.
 DE Bacillus subtilis Csa coding sequence SEQ ID NO:17.
 PN WO2003083125-A1.
 PD 09-OCT-2003.
 PA (GENV-) GENENCOR INT INC.
 Query Match 3.9%; Score 30.2; DB 10; Length 1353;
 Best Local Similarity 60.2%; Pred. No. 3e+02;
 RESULT 1312
 ID ADO26017 standard; DNA; 1508 BP.
 DE Cotton chalcone synthase (CHS) polynucleotide seqid 55.

PN WO2004046336-A2.
 PD 03-JUN-2004.
 PA (MONS-) MONSANTO TECHNOLOGY LLC.
 Query Match 3.9%; Score 30.2; DB 12; Length 1508;
 Best Local Similarity 58.2%; Pred. No. 3.2e+02;
 RESULT 1313
 ID ADA52483 standard; cDNA; 2624 BP.
 DE Human coding sequence, SEQ ID 51.
 PN EP1293569-A2.
 PD 19-MAR-2003.
 PA (HELI-) HELIX RES INST.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 3.9%; Score 30.2; DB 10; Length 2624;
 Best Local Similarity 51.9%; Pred. No. 4.1e+02;
 RESULT 1314
 ID AAH16320 standard; cDNA; 2687 BP.
 DE Human cDNA sequence SEQ ID NO:15219.
 PN EP1074617-A2.
 PD 07-FEB-2001.
 PA (HELI-) HELIX RES INST.
 Query Match 3.9%; Score 30.2; DB 4; Length 2687;
 Best Local Similarity 52.7%; Pred. No. 4.2e+02;
 RESULT 1315
 ID ADI21920 standard; cDNA; 2848 BP.
 DE Novel human protein cDNA #179.
 PN WO2003025148-A2.
 PD 27-MAR-2003.
 PA (HYSE-) HYSEQ INC.
 Query Match 3.9%; Score 30.2; DB 10; Length 2848;
 Best Local Similarity 53.9%; Pred. No. 4.3e+02;
 RESULT 1316
 ID ADQ22541 standard; DNA; 2938 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5361.
 PN WO2004048338-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 3.9%; Score 30.2; DB 12; Length 2938;
 Best Local Similarity 48.0%; Pred. No. 4.3e+02;
 RESULT 1317
 ID ABQ79969 standard; cDNA; 3535 BP.
 DE Human CD109 K15 variant protein encoding cDNA.
 PN WO200270696-A2.
 PD 12-SEP-2002.
 PA (SCHU/) SCHUH A.
 PA (SUTH/) SUTHERLAND R D.
 Query Match 3.9%; Score 30.2; DB 6; Length 3535;
 Best Local Similarity 48.0%; Pred. No. 4.7e+02;
 RESULT 1318
 ID ABQ79968 standard; cDNA; 3535 BP.
 DE Human CD109 K15 protein encoding cDNA.
 PN WO200270696-A2.
 PD 12-SEP-2002.
 PA (SCHU/) SCHUH A.
 PA (SUTH/) SUTHERLAND R D.
 Query Match 3.9%; Score 30.2; DB 6; Length 3535;
 Best Local Similarity 48.0%; Pred. No. 4.7e+02;
 RESULT 1319
 ID AAD49436 standard; DNA; 4146 BP.
 DE Human blood cell surface antigen, CD109 encoding DNA #1.
 PN WO200285942-A2.
 PD 31-OCT-2002.
 PA (UYMC-) UNIV MCGILL.
 Query Match 3.9%; Score 30.2; DB 8; Length 4146;
 Best Local Similarity 48.0%; Pred. No. 5.1e+02;
 RESULT 1320
 ID AAD49437 standard; DNA; 4197 BP.
 DE Human x150 DNA #2.
 PN WO200285942-A2.
 PD 31-OCT-2002.
 PA (UYMC-) UNIV MCGILL.
 Query Match 3.9%; Score 30.2; DB 8; Length 4197;
 Best Local Similarity 48.0%; Pred. No. 5.1e+02;
 RESULT 1321

ID AAF60199 standard; DNA; 4335 BP.
 DE Hydrophobic domain protein cDNA HP02837 isolated from HT-1080 cells.
 PN WO200029448-A2.
 PD 25-MAY-2000.
 PA (SAGA) SAGAMI CHEM RES CENT.
 PA (PROT-) PROTEGENE INC.
 Query Match 3.9%; Score 30.2; DB 3; Length 4335;
 Best Local Similarity 48.0%; Pred. No. 5.2e+02;
 RESULT 1322
 ID AAL49816 standard; cDNA; 4335 BP.
 DE Human platelet alloantigen Govb coding sequence.
 PN WO200270738-A2.
 PD 12-SEP-2002.
 PA (SCHU/) SCHUH A.
 Query Match 3.9%; Score 30.2; DB 6; Length 4335;
 Best Local Similarity 48.0%; Pred. No. 5.2e+02;
 RESULT 1323
 ID AAL49815 standard; cDNA; 4335 BP.
 DE Human platelet alloantigen Gova coding sequence.
 PN WO200270738-A2.
 PD 12-SEP-2002.
 PA (SCHU/) SCHUH A.
 Query Match 3.9%; Score 30.2; DB 6; Length 4335;
 Best Local Similarity 48.0%; Pred. No. 5.2e+02;
 RESULT 1324
 ID AAD49434 standard; DNA; 4369 BP.
 DE Human r150 gene #1.
 PN WO200285942-A2.
 PD 31-OCT-2002.
 PA (UYMC-) UNIV MCGILL.
 Query Match 3.9%; Score 30.2; DB 8; Length 4369;
 Best Local Similarity 48.0%; Pred. No. 5.2e+02;
 RESULT 1325
 ID AAF62010 standard; DNA; 4473 BP.
 DE Hydrophobic domain protein cDNA HP02837 isolated from HT-1080 cells.
 PN WO200029448-A2.
 PD 25-MAY-2000.
 PA (SAGA) SAGAMI CHEM RES CENT.
 PA (PROT-) PROTEGENE INC.
 Query Match 3.9%; Score 30.2; DB 3; Length 4473;
 Best Local Similarity 48.0%; Pred. No. 5.3e+02;
 RESULT 1326
 ID ABQ79964 standard; cDNA; 4761 BP.
 DE Human CD109 K1 protein encoding cDNA.
 PN WO200270696-A2.
 PD 12-SEP-2002.
 PA (SCHU/) SCHUH A.
 PA (SUTH/) SUTHERLAND R D.
 Query Match 3.9%; Score 30.2; DB 6; Length 4761;
 Best Local Similarity 48.0%; Pred. No. 5.4e+02;
 RESULT 1327
 ID ABQ79965 standard; cDNA; 4761 BP.
 DE Human CD109 K1 variant protein encoding cDNA.
 PN WO200270696-A2.
 PD 12-SEP-2002.
 PA (SCHU/) SCHUH A.
 PA (SUTH/) SUTHERLAND R D.
 Query Match 3.9%; Score 30.2; DB 6; Length 4761;
 Best Local Similarity 48.0%; Pred. No. 5.4e+02;
 RESULT 1328
 ID AAF4629 standard; cDNA; 4983 BP.
 DE Novel protein kinase cDNA, SEQ ID NO: 8.
 PN WO200073469-A2.
 PD 07-DEC-2000.
 PA (SUGE-) SUGEN INC.
 Query Match 3.9%; Score 30.2; DB 4; Length 4983;
 Best Local Similarity 55.1%; Pred. No. 5.5e+02;
 RESULT 1329
 ID AD129327 standard; cDNA; 4983 BP.
 DE Human MARK3-associated cDNA #6.
 PN US2003232771-A1.
 PD 18-DEC-2003.
 PA (ISIS-) ISIS PHARM INC.

Query Match 3.9%; Score 30.2; DB 12; Length 4983;
 Best Local Similarity 55.1%; Pred. No. 5.5e+02;
 RESULT 1330
 ID AAF30935 standard; cDNA; 5592 BP.
 DE Spodoptera frugiperda Bt toxin receptor cDNA.
 PN WO200136639-A2.
 PD 25-MAY-2001.
 PA (PION-) PIONEER HI-BRED INT INC.
 Query Match 3.9%; Score 30.2; DB 4; Length 5592;
 Best Local Similarity 52.0%; Pred. No. 5.9e+02;
 RESULT 1331
 ID AAD49440 standard; DNA; 5882 BP.
 DE Human blood cell surface antigen, CD109 encoding DNA #2.
 PN WO200285942-A2.
 PD 31-OCT-2002.
 PA (UYMC-) UNIV MCGILL.
 Query Match 3.9%; Score 30.2; DB 8; Length 5882;
 Best Local Similarity 48.0%; Pred. No. 6e+02;
 RESULT 1332
 ID AAD49435 standard; DNA; 5883 BP.
 DE Human r150 DNA #1.
 PN WO200285942-A2.
 PD 31-OCT-2002.
 PA (UYMC-) UNIV MCGILL.
 Query Match 3.9%; Score 30.2; DB 8; Length 5883;
 Best Local Similarity 48.0%; Pred. No. 6e+02;
 RESULT 1333
 ID ABQ79967 standard; cDNA; 5895 BP.
 DE Human CD109 K1-H7 variant protein encoding cDNA.
 PN WO200270696-A2.
 PD 12-SEP-2002.
 PA (SCHU/) SCHUH A.
 PA (SUTH/) SUTHERLAND R D.
 Query Match 3.9%; Score 30.2; DB 6; Length 5895;
 Best Local Similarity 48.0%; Pred. No. 6e+02;
 RESULT 1334
 ID ABQ79966 standard; cDNA; 5895 BP.
 DE Human CD109 K1-H7 protein encoding cDNA.
 PN WO200270696-A2.
 PD 12-SEP-2002.
 PA (SCHU/) SCHUH A.
 PA (SUTH/) SUTHERLAND R D.
 Query Match 3.9%; Score 30.2; DB 6; Length 5895;
 Best Local Similarity 48.0%; Pred. No. 6e+02;
 RESULT 1335
 ID AAS46515 standard; DNA; 5989 BP.
 DE Tumour suppressor gene derived chemically modified sequence #237.
 PN WO200168912-A2.
 PD 20-SEP-2001.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 3.9%; Score 30.2; DB 4; Length 5989;
 Best Local Similarity 62.7%; Pred. No. 6e+02;
 RESULT 1336
 ID AAS45476 standard; DNA; 6203 BP.
 DE Chemically pretreated genomic DNA associated with cell cycle #91.
 PN WO200168911-A2.
 PD 20-SEP-2001.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 3.9%; Score 30.2; DB 4; Length 6203;
 Best Local Similarity 49.7%; Pred. No. 6.1e+02;
 RESULT 1337
 ID ABK28400 standard; DNA; 6203 BP.
 DE DNA transcription associated complementary genomic DNA #137.
 PN WO200192565-A2.
 PD 06-DEC-2001.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 3.9%; Score 30.2; DB 6; Length 6203;
 Best Local Similarity 49.7%; Pred. No. 6.1e+02;
 RESULT 1338
 ID AAS93523 standard; cDNA; 7938 BP.
 DE DNA encoding novel human diagnostic protein #29327.
 PN WO200175067-A2.
 PD 11-OCT-2001.

PA (HYSE-) HYSEQ INC.
 Query Match 3.9%; Score 30.2; DB 5; Length 7938;
 Best Local Similarity 50.3%; Pred. No. 6.9e+02;
 RESULT 1339
 ID ADB54262 standard; DNA; 8244 BP.
 DE Pretreated genomic DNA region 186.
 PN WO2003072821-A2.
 PD 04-SEP-2003.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 3.9%; Score 30.2; DB 10; Length 8244;
 Best Local Similarity 51.1%; Pred. No. 7e+02;
 RESULT 1340
 ID ABU70228 standard; DNA; 8897 BP.
 DE Chemically treated cell signalling DNA sequence complementary to#59.
 PN WO200202807-A2.
 PD 10-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 3.9%; Score 30.2; DB 6; Length 8897;
 Best Local Similarity 50.3%; Pred. No. 7.3e+02;
 RESULT 1341
 ID AAS76397 standard; cDNA; 9223 BP.
 DE DNA encoding novel human diagnostic protein #12201.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 3.9%; Score 30.2; DB 5; Length 9223;
 Best Local Similarity 50.3%; Pred. No. 7.4e+02;
 RESULT 1342
 ID AAS59531 standard; DNA; 9292 BP.
 DE Propionibacterium acnes immunogenic protein encoding DNA #26.
 PN WO200181581-A2.
 PD 01-NOV-2001.
 PA (CORI-) CORIXA CORP.
 Query Match 3.9%; Score 30.2; DB 4; Length 9292;
 Best Local Similarity 62.7%; Pred. No. 7.4e+02;
 RESULT 1343
 ID ACF64460 standard; DNA; 9292 BP.
 DE Propionibacterium acnes DNA contig sequence #26.
 PN WO2003033515-A1.
 PD 24-APR-2003.
 PA (CORI-) CORIXA CORP.
 Query Match 3.9%; Score 30.2; DB 8; Length 9292;
 Best Local Similarity 62.7%; Pred. No. 7.4e+02;
 RESULT 1344
 ID ABL32895 standard; DNA; 11729 BP.
 DE Human immune system associated gene SEQ ID NO: 868.
 PN WO200200928-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 3.9%; Score 30.2; DB 6; Length 11729;
 Best Local Similarity 48.0%; Pred. No. 8.3e+02;
 RESULT 1345
 ID ABK31474 standard; DNA; 12584 BP.
 DE Signal transduction associated gene modified DNA #159.
 PN WO200200926-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 3.9%; Score 30.2; DB 6; Length 12584;
 Best Local Similarity 49.7%; Pred. No. 8.6e+02;
 RESULT 1346
 ID ABL70445 standard; DNA; 12584 BP.
 DE Chemically treated cell signalling DNA sequence#168.
 PN WO200202807-A2.
 PD 10-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 3.9%; Score 30.2; DB 6; Length 12584;
 Best Local Similarity 49.7%; Pred. No. 8.6e+02;
 RESULT 1347
 ID AAS61398 standard; DNA; 12584 BP.
 DE Human gene regulation-associated gene oligonucleotide #353.
 PN WO200177375-A2.
 PD 18-OCT-2001.
 PA (EPIG-) EPIGENOMICS AG.

Query Match 3.9%; Score 30.2; DB 6; Length 12584;
 Best Local Similarity 49.7%; Pred. No. 8.6e+02;
 RESULT 1348
 ID ABR80146 standard; DNA; 14920 BP.
 DE Human chemically modified disease associated gene SEQ ID NO 163.
 PN WO200200927-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 3.9%; Score 30.2; DB 6; Length 14920;
 Best Local Similarity 48.5%; Pred. No. 9.3e+02;
 RESULT 1349
 ID ABK39964 standard; DNA; 15479 BP.
 DE Human chemically pretreated gene sequence #23 strand 1.
 PN WO200202806-A2.
 PD 10-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 3.9%; Score 30.2; DB 6; Length 15479;
 Best Local Similarity 48.0%; Pred. No. 9.4e+02;
 RESULT 1350
 ID AAD19232 standard; DNA; 16545 BP.
 DE Human CG168 (or C595) receptor protein encoding DNA #2.
 PN WO200179446-A2.
 PD 25-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 3.9%; Score 30.2; DB 5; Length 16545;
 Best Local Similarity 51.9%; Pred. No. 9.7e+02;
 RESULT 1351
 ID ABK42737 standard; DNA; 20029 BP.
 DE Genomic sequence #636 encoding novel human connective tissue polypeptide.
 PN WO200155343-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 3.9%; Score 30.2; DB 9; Length 20029;
 Best Local Similarity 50.3%; Pred. No. 1.1e+03;
 RESULT 1352
 ID ADB60893 standard; DNA; 20029 BP.
 DE Connective tissue related genomic DNA #636.
 PN US2003054375-A1.
 PD 20-MAR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 3.9%; Score 30.2; DB 9; Length 20029;
 Best Local Similarity 50.3%; Pred. No. 1.1e+03;
 RESULT 1353
 ID ABQ80553 standard; DNA; 47841 BP.
 DE Human Canion gene fragment #3.
 PN WO200246404-A2.
 PD 13-JUN-2002.
 PA (GEST) GENSET.
 Query Match 3.9%; Score 30.2; DB 6; Length 47841;
 Best Local Similarity 46.8%; Pred. No. 1.6e+03;
 RESULT 1354
 ID AAZ10752 standard; DNA; 72604 BP.
 DE Genomic sequence of the human HKNG1 gene.
 PN WO9947535-A1.
 PD 23-SEP-1999.
 PA (MILL-) MILLENNIUM PHARM INC.
 (REGC) UNIV CALIFORNIA.
 Query Match 3.9%; Score 30.2; DB 2; Length 72604;
 Best Local Similarity 55.1%; Pred. No. 1.9e+03;
 RESULT 1355
 ID ABK43231 standard; DNA; 72604 BP.
 DE Human HKNG1 gene.
 PN WO200210366-A2.
 PD 07-FEB-2002.
 PA (MILL-) MILLENNIUM PHARM INC.
 (REGC) UNIV CALIFORNIA.
 Query Match 3.9%; Score 30.2; DB 6; Length 72604;
 Best Local Similarity 55.1%; Pred. No. 1.9e+03;
 RESULT 1356
 Query Match 3.9%; Score 30.2; DB 2; Length 110000;
 Best Local Similarity 58.2%; Pred. No. 2.3e+03;
 RESULT 1357
 Query Match 3.9%; Score 30.2; DB 6; Length 110000;

Best Local Similarity 53.9%; Pred. No. 2.3e+03;
RESULT 1358
ID ABK94701 standard; DNA; 323 BP.
DE Neurodegenerative disease associated polynucleotide #10.
PN WO200240996-A2.
PD 23-MAY-2002.
PA (MITO-) MITOKOR.
Query Match 3.9%; Score 30; DB 6; Length 323;
Best Local Similarity 52.4%; Pred. No. 1.8e+02;
RESULT 1359
ID ABX05956 standard; DNA; 327 BP.
DE S. pneumoniae type 4 strain coding region #244.
PN WO200272021-A2.
PD 03-OCT-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 3.9%; Score 30; DB 10; Length 327;
Best Local Similarity 59.3%; Pred. No. 1.8e+02;
RESULT 1360
ID AAC19546 standard; cDNA; 372 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 23621.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST-) GENSET.
Query Match 3.9%; Score 30; DB 3; Length 372;
Best Local Similarity 50.7%; Pred. No. 1.9e+02;
RESULT 1361
ID ABX41119 standard; cDNA; 375 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #6284.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT-) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 3.9%; Score 30; DB 8; Length 375;
Best Local Similarity 61.5%; Pred. No. 1.9e+02;
RESULT 1362
ID AAA28547 standard; DNA; 382 BP.
DE Human PC-1 gene intron 6/intron 7 partial sequences.
PN WO200029424-A1.
PD 25-MAY-2000.
PA (REGC-) UNIV CALIFORNIA.
PA (OSPE-) OSPEDALE CASA SOLLIEVO SOFFERENZA.
PA (UYCA-) UNIV DI CATANIA.
Query Match 3.9%; Score 30; DB 3; Length 382;
Best Local Similarity 59.3%; Pred. No. 1.9e+02;
RESULT 1363
ID AAL02343 standard; cDNA; 429 BP.
DE Human reproductive system related antigen cDNA SEQ ID NO: 2344.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.9%; Score 30; DB 4; Length 429;
Best Local Similarity 54.5%; Pred. No. 2e+02;
RESULT 1364
ID ABA07648 standard; cDNA; 429 BP.
DE Human ovarian and breast cancer associated polynucleotide SEQ ID NO 205.
PN WO200155325-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.9%; Score 30; DB 4; Length 429;
Best Local Similarity 54.5%; Pred. No. 2e+02;
RESULT 1365
ID AAA67557 standard; DNA; 470 BP.
DE Eucalyptus grandis transketolase DNA sequence SEQ ID NO:558.
PN WO200022092-A2.
PD 20-APR-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
Query Match 3.9%; Score 30; DB 3; Length 470;
Best Local Similarity 54.5%; Pred. No. 2.1e+02;
RESULT 1366
ID ABL16003 standard; cDNA; 475 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 42491.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 3.9%; Score 30; DB 4; Length 475;
Best Local Similarity 64.3%; Pred. No. 2.1e+02;
RESULT 1367
ID ABN61741 standard; cDNA; 594 BP.
DE Human cancer related polynucleotide SEQ ID NO 1708.
PN WO200214500-A2.
PD 21-FEB-2002.
PA (CHIR-) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 3.9%; Score 30; DB 6; Length 594;
Best Local Similarity 61.5%; Pred. No. 2.4e+02;
RESULT 1368
ID ACA27794 standard; DNA; 651 BP.
DE Prokaryotic essential gene #9451.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 3.9%; Score 30; DB 8; Length 651;
Best Local Similarity 48.3%; Pred. No. 2.5e+02;
RESULT 1369
ID AAH51629 standard; cDNA; 838 BP.
DE Human g35018 cDNA sequence SEQ ID 38.
PN WO200058510-A2.
PD 05-OCT-2000.
PA (GEST-) GENSET.
Query Match 3.9%; Score 30; DB 3; Length 838;
Best Local Similarity 52.4%; Pred. No. 2.8e+02;
RESULT 1370
ID ABN74609 standard; cDNA; 931 BP.
DE Bovine embryonic germ (EG) cell cDNA EST #660.
PN WO200194550-A2.
PD 13-DEC-2001.
PA (INFI-) INFIGEN INC.
Query Match 3.9%; Score 30; DB 6; Length 931;
Best Local Similarity 46.8%; Pred. No. 2.9e+02;
RESULT 1371
ID AAH51630 standard; cDNA; 985 BP.
DE Human g35018 cDNA sequence SEQ ID 39.
PN WO200058510-A2.
PD 05-OCT-2000.
PA (GEST-) GENSET.
Query Match 3.9%; Score 30; DB 3; Length 985;
Best Local Similarity 52.4%; Pred. No. 3e+02;
RESULT 1372
ID ABZ83299 standard; cDNA; 1024 BP.
DE Toxicologically relevant human nucleotide sequence #458.
PN WO2003016500-A2.
PD 27-FEB-2003.
PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
Query Match 3.9%; Score 30; DB 10; Length 1024;
Best Local Similarity 52.4%; Pred. No. 3e+02;
RESULT 1373
ID ABL28745 standard; DNA; 1047 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 37708.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 3.9%; Score 30; DB 4; Length 1047;
Best Local Similarity 64.3%; Pred. No. 3.1e+02;
RESULT 1374
ID ABL64399 standard; DNA; 1052 BP.
DE Stomach cancer related gene sequence SEQ ID NO:2736.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 3.9%; Score 30; DB 6; Length 1052;
Best Local Similarity 52.4%; Pred. No. 3.1e+02;
RESULT 1375

ID ABX95118 standard; DNA; 1070 BP.
DE DNA sequence encoding human Biliverdin reductase (BVR) 1 protein.
PN US2003027124-A1.
PD 06-FEB-2003.
PA (MAIN/) MAINES M D.
Query Match 3.9%; Score 30; DB 8; Length 1070;
Best Local Similarity 52.4%; Pred. No. 3.1e+02;
RESULT 1376
ID ACF05667 standard; DNA; 1070 BP.
DE Human biliverdin reductase DNA.
PN WO2003055981-A2.
PD 10-JUL-2003.
PA (UTRP) UNIV ROCHESTER.
Query Match 3.9%; Score 30; DB 9; Length 1070;
Best Local Similarity 52.4%; Pred. No. 3.1e+02;
RESULT 1377
ID AAH51628 standard; cDNA; 1154 BP.
DE Human g35018 cDNA sequence SEQ ID 37.
PN WO200058510-A2.
PD 05-OCT-2000.
PA (GEST) GENSET.
Query Match 3.9%; Score 30; DB 3; Length 1154;
Best Local Similarity 52.4%; Pred. No. 3.2e+02;
RESULT 1378
ID ADH82989 standard; DNA; 1236 BP.
DE Enterococcus faecalis polynucleotide #874.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 3.9%; Score 30; DB 10; Length 1236;
Best Local Similarity 46.6%; Pred. No. 3.3e+02;
RESULT 1379
ID AAH51627 standard; cDNA; 1301 BP.
DE Human g35018 cDNA sequence SEQ ID 36.
PN WO200058510-A2.
PD 05-OCT-2000.
PA (GEST) GENSET.
Query Match 3.9%; Score 30; DB 3; Length 1301;
Best Local Similarity 52.4%; Pred. No. 3.4e+02;
RESULT 1380
ID AAZ97063 standard; cDNA; 1357 BP.
DE Human secreted protein gene 45 cDNA clone HAGDI35, SEQ ID NO:55.
PN WO9966041-A1.
PD 23-DEC-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.9%; Score 30; DB 3; Length 1357;
Best Local Similarity 45.9%; Pred. No. 3.5e+02;
RESULT 1381
ID ADA39642 standard; cDNA; 1357 BP.
DE Human secreted protein encoding cDNA.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.9%; Score 30; DB 8; Length 1357;
Best Local Similarity 45.9%; Pred. No. 3.5e+02;
RESULT 1382
ID ACH66692 standard; cDNA; 1357 BP.
DE Novel human secreted protein #45 cDNA.
PN US2003065151-A1.
PD 03-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.9%; Score 30; DB 9; Length 1357;
Best Local Similarity 45.9%; Pred. No. 3.5e+02;
RESULT 1383
ID ADC73388 standard; DNA; 1357 BP.
DE Human secreted protein-related DNA - SEQ ID 21.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.9%; Score 30; DB 10; Length 1357;
Best Local Similarity 45.9%; Pred. No. 3.5e+02;
RESULT 1384

ID AAH51631 standard; cDNA; 1386 BP.
DE Human g35018 cDNA sequence SEQ ID 40.
PN WO200058510-A2.
PD 05-OCT-2000.
PA (GEST) GENSET.
Query Match 3.9%; Score 30; DB 3; Length 1386;
Best Local Similarity 52.4%; Pred. No. 3.5e+02;
RESULT 1385
ID AAH72858 standard; cDNA; 1445 BP.
DE Human cervical cancer marker nucleic acid 4132.
PN WO200142467-A2.
PD 14-JUN-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.9%; Score 30; DB 4; Length 1445;
Best Local Similarity 57.4%; Pred. No. 3.6e+02;
RESULT 1386
ID ADL62765 standard; DNA; 1445 BP.
DE Human ovarian cancer DNA marker #20977.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.9%; Score 30; DB 5; Length 1445;
Best Local Similarity 57.4%; Pred. No. 3.6e+02;
RESULT 1387
ID AAF32772 standard; cDNA; 1578 BP.
DE Human secreted protein cDNA #16.
PN WO200077197-A1.
PD 21-DEC-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match 3.9%; Score 30; DB 4; Length 1578;
Best Local Similarity 50.0%; Pred. No. 3.7e+02;
RESULT 1388
ID ABL09057 standard; cDNA; 1645 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 21653.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.9%; Score 30; DB 4; Length 1645;
Best Local Similarity 48.3%; Pred. No. 3.8e+02;
RESULT 1389
ID ADQ22866 standard; DNA; 1675 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5686.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 3.9%; Score 30; DB 12; Length 1675;
Best Local Similarity 50.7%; Pred. No. 3.8e+02;
RESULT 1390
ID AAL06896 standard; DNA; 1880 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 9584.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.9%; Score 30; DB 4; Length 1880;
Best Local Similarity 54.5%; Pred. No. 4e+02;
RESULT 1391
ID AAL06897 standard; DNA; 1880 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 9585.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.9%; Score 30; DB 4; Length 1880;
Best Local Similarity 54.5%; Pred. No. 4e+02;
RESULT 1392
ID ABA08116 standard; DNA; 1880 BP.
DE Human ovarian and breast cancer associated polynucleotide SEQ ID NO 911.
PN WO200155325-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.9%; Score 30; DB 4; Length 1880;
Best Local Similarity 54.5%; Pred. No. 4e+02;
RESULT 1393

ID ABA08115 standard; DNA; 1880 BP.
DE Human ovarian and breast cancer associated polynucleotide SEQ ID NO 910.
PN WO200155325-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.9%; Score 30; DB 4; Length 1880;
Best Local Similarity 54.5%; Pred. No. 4e+02;
RESULT 1394
ID ADA73281 standard; DNA; 2000 BP.
DE Rice gene, SEQ ID 6607.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 3.9%; Score 30; DB 8; Length 2000;
Best Local Similarity 67.7%; Pred. No. 4.2e+02;
RESULT 1395
ID ADJ41527 standard; cDNA; 2000 BP.
DE Plant cDNA #2527.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW) BUDWORTH P.
PA (MOUG) MOUGHAMER T.
PA (BRIG) BRIGGS S P.
PA (COOP) COOPER B.
PA (GLAZ) GLAZEBROOK J.
PA (GOFF) GOFF S A.
PA (KATA) KATAGIRI F.
PA (KREP) KREPS J.
PA (PROV) PROVART N.
PA (RICK) RICHE D.
PA (ZHU) ZHU T.
Query Match 3.9%; Score 30; DB 12; Length 2000;
Best Local Similarity 52.4%; Pred. No. 4.2e+02;
RESULT 1396
ID ADA31173 standard; DNA; 2007 BP.
DE DNA encoding Acinetobacter baumannii protein #2460.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 3.9%; Score 30; DB 9; Length 2007;
Best Local Similarity 51.5%; Pred. No. 4.2e+02;
RESULT 1397
ID ADQ24884 standard; DNA; 2291 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7704.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 3.9%; Score 30; DB 12; Length 2291;
Best Local Similarity 50.7%; Pred. No. 4.4e+02;
RESULT 1398
ID AAK81968 standard; DNA; 2514 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36780.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.9%; Score 30; DB 4; Length 2514;
Best Local Similarity 57.4%; Pred. No. 4.6e+02;
RESULT 1399
ID ADO61722 standard; DNA; 2721 BP.
DE Transcription factor G1206 coding sequence, SEQ ID 189.
PN WO2004031349-A2.
PD 15-APR-2004.
PA (MENDE-) MENDEL BIOTECHNOLOGY INC.
Query Match 3.9%; Score 30; DB 12; Length 2721;
Best Local Similarity 54.5%; Pred. No. 4.8e+02;
RESULT 1400
ID ABL17175 standard; DNA; 2980 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 3244.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.9%; Score 30; DB 4; Length 2830;
Best Local Similarity 48.3%; Pred. No. 4.9e+02;

RESULT 1401
ID ABL17175 standard; DNA; 2980 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 2998.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.9%; Score 30; DB 4; Length 2980;
Best Local Similarity 48.3%; Pred. No. 5e+02;
RESULT 1402
ID ABL16002 standard; cDNA; 3195 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 42488.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.9%; Score 30; DB 4; Length 3195;
Best Local Similarity 64.3%; Pred. No. 5.2e+02;
RESULT 1403
ID AAF16145 standard; cDNA; 4006 BP.
DE Human prostate cancer antigen nucleotide sequence SEQ ID NO:580.
PN WO200055174-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE) ROSEN C A.
Query Match 3.9%; Score 30; DB 3; Length 4006;
Best Local Similarity 45.9%; Pred. No. 5.8e+02;
RESULT 1404
ID ABA07203 standard; DNA; 4338 BP.
DE Human pancreatic cancer related genomic DNA, SEQ ID NO: 522.
PN WO200155206-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.9%; Score 30; DB 4; Length 4338;
Best Local Similarity 61.5%; Pred. No. 6e+02;
RESULT 1405
ID AAK89835 standard; DNA; 4338 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 3411.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.9%; Score 30; DB 4; Length 4338;
Best Local Similarity 61.5%; Pred. No. 6e+02;
RESULT 1406
ID ABA06871 standard; DNA; 4338 BP.
DE Human polynucleotide SEQ ID NO 27.
PN WO200155205-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.9%; Score 30; DB 4; Length 4338;
Best Local Similarity 61.5%; Pred. No. 6e+02;
RESULT 1407
ID ACA61956 standard; DNA; 4338 BP.
DE DNA encoding human HVADT77 protein #1.
PN US2003044890-A1.
PD 06-MAR-2003.
PA (ROSE) ROSEN C A.
PA (RUBE) RUBEN S M.
PA (BARA) BARASH S C.
Query Match 3.9%; Score 30; DB 10; Length 4338;
Best Local Similarity 61.5%; Pred. No. 6e+02;
RESULT 1408
ID ABL09056 standard; cDNA; 4408 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 21650.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.9%; Score 30; DB 4; Length 4408;
Best Local Similarity 48.3%; Pred. No. 6e+02;
RESULT 1409
ID AAK75249 standard; DNA; 4447 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:30061.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 3.9%; Score 30; DB 4; Length 4447;
 Best Local Similarity 57.4%; Pred. No. 6e+02;
 RESULT 1410
 ID ABL17256 standard; DNA; 5367 BP.
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 3241.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 3.9%; Score 30; DB 4; Length 5367;
 Best Local Similarity 48.3%; Pred. No. 6.6e+02;
 RESULT 1411
 ID ABL17174 standard; DNA; 5397 BP.
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 2995.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 3.9%; Score 30; DB 4; Length 5397;
 Best Local Similarity 48.3%; Pred. No. 6.6e+02;
 RESULT 1412
 ID ABL29956 standard; DNA; 6429 BP.
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 41341.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 3.9%; Score 30; DB 4; Length 6429;
 Best Local Similarity 57.4%; Pred. No. 7.2e+02;
 RESULT 1413
 ID ABL15594 standard; cDNA; 6436 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 41264.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 3.9%; Score 30; DB 4; Length 6436;
 Best Local Similarity 57.4%; Pred. No. 7.2e+02;
 RESULT 1414
 ID AAV52144 standard; DNA; 8148 BP.
 DE Streptococcus pneumoniae genome fragment SEQ ID NO:11.
 PN WO9818931-A2.
 PD 07-MAY-1998.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 3.9%; Score 30; DB 2; Length 8148;
 Best Local Similarity 59.3%; Pred. No. 8e+02;
 RESULT 1415
 ID ABL32113 standard; DNA; 9927 BP.
 DE Human immune system associated gene SEQ ID NO: 86.
 PN WO200200928-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 3.9%; Score 30; DB 6; Length 9927;
 Best Local Similarity 50.0%; Pred. No. 8.8e+02;
 RESULT 1416
 ID AAX13081 standard; DNA; 12860 BP.
 DE Enterococcus faecalis genome contig SEQ ID NO:144.
 PN WO9850555-A2.
 PD 12-NOV-1998.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 3.9%; Score 30; DB 2; Length 12860;
 Best Local Similarity 46.6%; Pred. No. 9.9e+02;
 RESULT 1417
 ID ABS98876 standard; DNA; 12860 BP.
 DE Enterococcus faecalis contig sequence #144.
 PN US2002120116-A1.
 PD 29-AUG-2002.
 PA (KUNS/) KONSCH C A.
 PA (DILL/) DILLON P J.
 PA (BARA/) BARASH S.
 Query Match 3.9%; Score 30; DB 6; Length 12860;
 Best Local Similarity 46.6%; Pred. No. 9.9e+02;
 RESULT 1418
 ID ABL28744 standard; DNA; 14197 BP.
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 37705.
 PN WO200171042-A2.
 PD 27-SEP-2001.

PA (PEKE) PE CORP NY.
 Query Match 3.9%; Score 30; DB 4; Length 14197;
 Best Local Similarity 64.3%; Pred. No. 1e+03;
 RESULT 1419
 ID AAK73103 standard; DNA; 15196 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27915.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 3.9%; Score 30; DB 4; Length 15196;
 Best Local Similarity 59.3%; Pred. No. 1.1e+03;
 RESULT 1420
 ID AAK87548 standard; DNA; 15196 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:42360.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 3.9%; Score 30; DB 4; Length 15196;
 Best Local Similarity 59.3%; Pred. No. 1.1e+03;
 RESULT 1421
 ID ABL32313 standard; DNA; 18683 BP.
 DE Human immune system associated gene SEQ ID NO: 286.
 PN WO200200928-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 3.9%; Score 30; DB 6; Length 18683;
 Best Local Similarity 47.0%; Pred. No. 1.2e+03;
 RESULT 1422
 ID ABL54334 standard; DNA; 18683 BP.
 DE Chemically treated apoptosis gene complementary to gene #17.
 PN WO200177164-A2.
 PD 18-OCT-2001.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 3.9%; Score 30; DB 6; Length 18683;
 Best Local Similarity 47.0%; Pred. No. 1.2e+03;
 RESULT 1423
 ID ADO79402 standard; DNA; 76600 BP.
 DE DLGI region, SEQ ID 1.
 PN WO2004047514-A2.
 PD 10-JUN-2004.
 PA (SEQU-) SEQUENOM INC.
 Query Match 3.9%; Score 30; DB 12; Length 76600;
 Best Local Similarity 50.0%; Pred. No. 2.3e+03;
 RESULT 1424
 Query Match 3.9%; Score 30; DB 12; Length 89378;
 Best Local Similarity 61.5%; Pred. No. 2.4e+03;
 RESULT 1425
 Query Match 3.9%; Score 30; DB 12; Length 89378;
 Best Local Similarity 61.5%; Pred. No. 2.4e+03;
 RESULT 1426
 Query Match 3.9%; Score 30; DB 12; Length 89378;
 Best Local Similarity 61.5%; Pred. No. 2.4e+03;
 RESULT 1427
 Query Match 3.9%; Score 30; DB 6; Length 110000;
 Best Local Similarity 47.8%; Pred. No. 2.6e+03;
 RESULT 1428
 Query Match 3.9%; Score 30; DB 10; Length 110000;
 Best Local Similarity 59.3%; Pred. No. 2.6e+03;
 RESULT 1429
 ID ADN47591 standard; DNA; 2089378 BP.
 DE Thermococcus kodakaraensis KOD1 genome DNA sequence SeqID1459.
 PN WO2004022736-A1.
 PD 18-MAR-2004.
 PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 Query Match 3.9%; Score 30; DB 12; Length 110000;
 Best Local Similarity 61.5%; Pred. No. 2.6e+03;
 RESULT 1430
 ID ADN47209 standard; DNA; 2089378 BP.
 DE Thermococcus kodakaraensis KOD1 genome DNA sequence SeqID1087.
 PN WO2004022736-A1.
 PD 18-MAR-2004.
 PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 Query Match 3.9%; Score 30; DB 12; Length 110000;

Best Local Similarity 61.5%; Pred. No. 2.6e+03;
 RESULT 1431
 ID ADN47960 standard; DNA; 2089378 BP.
 DE Thermococcus kodakaraensis KOD1 genome DNA sequence SeqID1838.
 PN WO2004022736-A1.
 PD 18-MAR-2004.
 PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 Query Match 3.9%; Score 30; DB 12; Length 110000;
 Best Local Similarity 61.5%; Pred. No. 2.6e+03;
 RESULT 1432
 ID ABK83461 standard; cDNA; 128600 BP.
 DE Human cDNA differentially expressed in granulocytic cells #32.
 PN WO200228999-A2.
 PD 11-APR-2002.
 PA (GENE-) GENE LOGIC INC.
 Query Match 3.9%; Score 30; DB 6; Length 128600;
 Best Local Similarity 50.7%; Pred. No. 2.8e+03;
 RESULT 1433
 ID ABR83574 standard; cDNA; 147419 BP.
 DE Human cDNA differentially expressed in granulocytic cells #145.
 PN WO200228999-A2.
 PD 11-APR-2002.
 PA (GENE-) GENE LOGIC INC.
 Query Match 3.9%; Score 30; DB 6; Length 147419;
 Best Local Similarity 51.5%; Pred. No. 3e+03;
 RESULT 1434
 ID ADG86300 standard; DNA; 220756 BP.
 DE Human SMRT partial genomic DNA sequence SEQ ID NO:14.
 PN WO2003106645-A2.
 PD 24-DEC-2003.
 PA (ISIS-) ISIS PHARM INC.
 Query Match 3.9%; Score 30; DB 12; Length 220756;
 Best Local Similarity 50.7%; Pred. No. 3.5e+03;
 RESULT 1435
 ID ADD25213 standard; DNA; 271990 BP.
 DE Fertility restorer protein genomic DNA sequence.
 PN WO2003006622-A2.
 PD 23-JAN-2003.
 PA (UYMC-) UNIV MCGILL.
 PA (DNAL-) DNA LANDMARKS INC.
 Query Match 3.9%; Score 30; DB 10; Length 271990;
 Best Local Similarity 59.3%; Pred. No. 3.7e+03;
 RESULT 1436
 ID ADN61228 standard; DNA; 271990 BP.
 DE Radish nuclear fertility restorer Rfo locus SEQ ID NO:87.
 PN WO2004006655-A2.
 PD 22-JAN-2004.
 PA (UYMC-) UNIV MCGILL.
 PA (DNAL-) DNA LANDMARKS INC.
 PA (BADI) BASF PLANT SCI GMBH.
 Query Match 3.9%; Score 30; DB 12; Length 271990;
 Best Local Similarity 59.3%; Pred. No. 3.7e+03;
 RESULT 1437
 ID AAH51601 standard; DNA; 319608 BP.
 DE Human chromosome 13q31-q33 genomic nucleotide sequence.
 PN WO200058510-A2.
 PD 05-OCT-2000.
 PA (GEST-) GENSET.
 Query Match 3.9%; Score 30; DB 3; Length 319608;
 Best Local Similarity 52.4%; Pred. No. 3.9e+03;
 RESULT 1438
 ID AAS09301 standard; DNA; 319608 BP.
 DE Human schizophrenia associated gene q35030 and biallelic markers A1-A71.
 Query Match 3.9%; Score 30; DB 5; Length 319608;
 Best Local Similarity 52.4%; Pred. No. 3.9e+03;
 RESULT 1439
 ID ABX89084 standard; cDNA; 298 BP.
 DE Corn ear-derived polynucleotide (cpd) #7544.
 PN US6476212-B1.
 PD 05-NOV-2002.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 3.9%; Score 29.8; DB 10; Length 298;
 Best Local Similarity 60.5%; Pred. No. 2e+02;

RESULT 1440
 ID ABV11776 standard; cDNA; 377 BP.
 DE Human prostate expression marker cDNA 11767.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 3.9%; Score 29.8; DB 5; Length 377;
 Best Local Similarity 52.9%; Pred. No. 2.2e+02;
 RESULT 1441
 ID AAK67152 standard; DNA; 405 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21964.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 3.9%; Score 29.8; DB 4; Length 405;
 Best Local Similarity 45.8%; Pred. No. 2.3e+02;
 RESULT 1442
 ID ABV32921 standard; cDNA; 417 BP.
 DE Human prostate expression marker cDNA 32912.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 3.9%; Score 29.8; DB 5; Length 417;
 Best Local Similarity 52.9%; Pred. No. 2.3e+02;
 RESULT 1443
 ID ABV86769 standard; cDNA; 434 BP.
 DE Human colon cancer related cDNA SEQ ID NO 80.
 PN WO200258534-A2.
 PD 01-AUG-2002.
 PA (CORI-) CORIXA CORP.
 Query Match 3.9%; Score 29.8; DB 6; Length 434;
 Best Local Similarity 55.2%; Pred. No. 2.3e+02;
 RESULT 1444
 ID ABV86980 standard; cDNA; 519 BP.
 DE Human colon cancer related cDNA SEQ ID NO 291.
 PN WO200258534-A2.
 PD 01-AUG-2002.
 PA (CORI-) CORIXA CORP.
 Query Match 3.9%; Score 29.8; DB 6; Length 519;
 Best Local Similarity 55.2%; Pred. No. 2.5e+02;
 RESULT 1445
 ID AA16422 standard; DNA; 567 BP.
 DE Human colon cancer differentially expressed nucleotide sequence #427.
 PN WO200012702-A2.
 PD 09-MAR-2000.
 PA (PARB) BAYER CORP.
 Query Match 3.9%; Score 29.8; DB 3; Length 567;
 Best Local Similarity 59.7%; Pred. No. 2.7e+02;
 RESULT 1446
 ID ABV87337 standard; cDNA; 580 BP.
 DE Human colon cancer related cDNA SEQ ID NO 648.
 PN WO200258534-A2.
 PD 01-AUG-2002.
 PA (CORI-) CORIXA CORP.
 Query Match 3.9%; Score 29.8; DB 6; Length 580;
 Best Local Similarity 55.2%; Pred. No. 2.7e+02;
 RESULT 1447
 ID AAC53674 standard; DNA; 678 BP.
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 75318.
 PN EPI033405-A2.
 PD 06-SEP-2000.
 Query Match 3.9%; Score 29.8; DB 3; Length 678;
 Best Local Similarity 47.2%; Pred. No. 2.9e+02;
 RESULT 1448
 ID ADI30720 standard; cDNA; 704 BP.
 DE Human cDNA #46.
 PN US6607879-B1.
 PD 19-AUG-2003.
 PA (INCY-) INCYTE CORP.
 Query Match 3.9%; Score 29.8; DB 11; Length 704;
 Best Local Similarity 50.4%; Pred. No. 2.9e+02;
 RESULT 1449
 ID AAI95633 standard; cDNA; 757 BP.

DE Human neuroblastoma expressed polynucleotide SEQ ID NO 1708.
PN WO200166719-A1.
PD 13-SEP-2001.
PA (CHIB-) CHIBA PREFECTURE.
PA (HISM-) HISAMITSU PHARM CO LTD.
Query Match 3.9%; Score 29.8; DB 4; Length 757;
Best Local Similarity 58.4%; Pred. No. 3e+02;
RESULT 1450
ID AAZ15504 standard; cDNA; 760 BP.
DE Human gene expression product cDNA sequence SEQ ID NO:2973.
PN WO9339572-A2.
PD 05-AUG-1999.
PA (CHIR-) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 3.9%; Score 29.8; DB 2; Length 760;
Best Local Similarity 55.0%; Pred. No. 3e+02;
RESULT 1451
ID ABV05980 standard; cDNA; 833 BP.
DE Human prostate expression marker cDNA 5971.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.9%; Score 29.8; DB 5; Length 833;
Best Local Similarity 44.1%; Pred. No. 3.2e+02;
RESULT 1452
ID AAC34752 standard; DNA; 902 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 7764.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 3.9%; Score 29.8; DB 3; Length 902;
Best Local Similarity 51.1%; Pred. No. 3.3e+02;
RESULT 1453
ID ABQ33943 standard; DNA; 1126 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 20534.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.9%; Score 29.8; DB 6; Length 1126;
Best Local Similarity 49.7%; Pred. No. 3.7e+02;
RESULT 1454
ID ABQ33942 standard; DNA; 1126 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 20533.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.9%; Score 29.8; DB 6; Length 1126;
Best Local Similarity 49.7%; Pred. No. 3.7e+02;
RESULT 1455
ID ADD49054 standard; DNA; 1157 BP.
DE Human NOV7a coding sequence, SEQ ID 27.
PN WO2003060149-A2.
PD 24-JUL-2003.
PA (CURA-) CURAGEN CORP.
Query Match 3.9%; Score 29.8; DB 10; Length 1157;
Best Local Similarity 55.2%; Pred. No. 3.7e+02;
RESULT 1456
ID AAC37127 standard; DNA; 1213 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 16274.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 3.9%; Score 29.8; DB 3; Length 1213;
Best Local Similarity 51.1%; Pred. No. 3.8e+02;
RESULT 1457
ID ADJ75145 standard; DNA; 1310 BP.
DE Marker gene SEQ ID NO:397.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 3.9%; Score 29.8; DB 12; Length 1310;
Best Local Similarity 55.2%; Pred. No. 3.9e+02;
RESULT 1458
ID ADN04566 standard; cDNA; 1310 BP.
DE Antiporiatic cDNA sequence #487.
PN WO200171042-A2.

PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH-) GENENTECH INC.
Query Match 3.9%; Score 29.8; DB 12; Length 1310;
Best Local Similarity 55.2%; Pred. No. 3.9e+02;
RESULT 1459
ID AAQ75377 standard; DNA; 1316 BP.
DE Human elastase inhibitor gene.
PN US5370991-A.
PD 06-DEC-1994.
PA (BLOO-) CENT BLOOD RES INC.
Query Match 3.9%; Score 29.8; DB 2; Length 1316;
Best Local Similarity 55.2%; Pred. No. 3.9e+02;
RESULT 1460
ID AAT14255 standard; cDNA; 1316 BP.
DE Human elastase inhibitor cDNA.
PN WO9610418-A1.
PD 11-APR-1996.
PA (BLOO-) CENT BLOOD RES INC.
Query Match 3.9%; Score 29.8; DB 2; Length 1316;
Best Local Similarity 55.2%; Pred. No. 3.9e+02;
RESULT 1461
ID ABU69984 standard; DNA; 1316 BP.
DE Pancreas cancer related gene sequence SEQ ID NO:8321.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 3.9%; Score 29.8; DB 6; Length 1316;
Best Local Similarity 55.2%; Pred. No. 3.9e+02;
RESULT 1462
ID ABR84121 standard; cDNA; 1316 BP.
DE Human cDNA differentially expressed in granulocytic cells #692.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 3.9%; Score 29.8; DB 6; Length 1316;
Best Local Similarity 55.2%; Pred. No. 3.9e+02;
RESULT 1463
ID ACA56112 standard; cDNA; 1430 BP.
DE Horze signalling pathway polynucleotide probe SEQ ID NO 710.
PN US6500938-B1.
PD 31-DEC-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 3.9%; Score 29.8; DB 10; Length 1430;
Best Local Similarity 55.2%; Pred. No. 4.1e+02;
RESULT 1464
ID ADI55908 standard; DNA; 1430 BP.
DE Human polynucleotide probe #710.
PN US2004010136-A1.
PD 15-JAN-2004.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 3.9%; Score 29.8; DB 12; Length 1430;
Best Local Similarity 55.2%; Pred. No. 4.1e+02;
RESULT 1465
ID ABZ35236 standard; cDNA; 1458 BP.
DE Human gene expression profile polynucleotide SEQ ID NO 347.
PN WO200274979-A2.
PD 26-SEP-2002.
PA (ORTH-) ORTHO CLINICAL DIAGNOSTICS INC.
Query Match 3.9%; Score 29.8; DB 6; Length 1458;
Best Local Similarity 55.2%; Pred. No. 4.1e+02;
RESULT 1466
ID ADD49056 standard; DNA; 1550 BP.
DE Human NOV7b coding sequence, SEQ ID 29.
PN WO2003060149-A2.
PD 24-JUL-2003.
PA (CURA-) CURAGEN CORP.
Query Match 3.9%; Score 29.8; DB 10; Length 1550;
Best Local Similarity 55.2%; Pred. No. 4.2e+02;
RESULT 1467
ID ABL27423 standard; DNA; 1596 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 33742.
PN WO200171042-A2.

PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.9%; Score 29.8; DB 4; Length 1596;
Best Local Similarity 58.4%; Pred. No. 4.3e+02;
RESULT 1468
ID ADF81744 standard; DNA; 1829 BP.
DE Leukaemia-related DNA sequence #2300.
PD WO2003039443-A2.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PD 15-MAY-2003.
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
PA (HAPE/) HAERLACH T.
PA (SCHO/) SCHOCH C.
PA (KERN/) KERN W.
Query Match 3.9%; Score 29.8; DB 10; Length 1829;
Best Local Similarity 55.2%; Pred. No. 4.6e+02;
RESULT 1469
ID AAC77964 standard; cDNA; 1931 BP.
DE Human cancer associated gene sequence SEQ ID NO:358.
PD WO200055350-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.9%; Score 29.8; DB 3; Length 1931;
Best Local Similarity 55.2%; Pred. No. 4.7e+02;
RESULT 1470
ID ADN04631 standard; cDNA; 2634 BP.
DE Antiporiatric cDNA sequence #525.
PD WO2004028479-A2.
PD 08-APR-2004.
PA (GFTH) GENENTECH INC.
Query Match 3.9%; Score 29.8; DB 12; Length 2634;
Best Local Similarity 55.2%; Pred. No. 5.4e+02;
RESULT 1471
ID ADJ58237 standard; DNA; 2883 BP.
DE Urease subunit polypeptide complex encoding sequence.
PD EP1176192-A2.
PD 30-JAN-2002.
PA (ALUK) AKZO NOBEL NV.
Query Match 3.9%; Score 29.8; DB 7; Length 2883;
Best Local Similarity 51.9%; Pred. No. 5.7e+02;
RESULT 1472
ID ABS53210 standard; cDNA; 3497 BP.
DE Human mitogen-activated protein kinase kinase (MKK) 4alpha cDNA.
PD US2002102691-A1.
PD 01-AUG-2002.
PA (UYMA-) UNIV MASSACHUSETTS.
Query Match 3.9%; Score 29.8; DB 6; Length 3497;
Best Local Similarity 46.4%; Pred. No. 6.2e+02;
RESULT 1473
ID ABL27422 standard; DNA; 3596 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 33739.
PD WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.9%; Score 29.8; DB 4; Length 3596;
Best Local Similarity 58.4%; Pred. No. 6.3e+02;
RESULT 1474
ID ABL02829 standard; cDNA; 3831 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 2969.
PD WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.9%; Score 29.8; DB 4; Length 3831;
Best Local Similarity 52.9%; Pred. No. 6.5e+02;
RESULT 1475
ID ABA09585 standard; DNA; 4464 BP.
DE Human bone marrow expressed oligonucleotide SEQ ID NO: 11.
PD WO200174836-A1.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 3.9%; Score 29.8; DB 5; Length 4464;
Best Local Similarity 51.1%; Pred. No. 7e+02;
RESULT 1476

ID ABA09669 standard; DNA; 4485 BP.
DE Human bone marrow expressed oligonucleotide SEQ ID NO: 178.
PD WO200174836-A1.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 3.9%; Score 29.8; DB 5; Length 4485;
Best Local Similarity 51.1%; Pred. No. 7e+02;
RESULT 1477
ID ABL20936 standard; DNA; 4747 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 14281.
PD WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.9%; Score 29.8; DB 4; Length 4747;
Best Local Similarity 56.7%; Pred. No. 7.2e+02;
RESULT 1478
ID AAK78479 standard; DNA; 4807 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33291.
PD WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.9%; Score 29.8; DB 4; Length 4807;
Best Local Similarity 49.8%; Pred. No. 7.2e+02;
RESULT 1479
ID AEN80116 standard; DNA; 6036 BP.
DE Human chemically modified disease associated gene SEQ ID NO 133.
PD WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.9%; Score 29.8; DB 6; Length 6036;
Best Local Similarity 55.2%; Pred. No. 8e+02;
RESULT 1480
ID ABL02828 standard; cDNA; 6103 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 2966.
PD WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.9%; Score 29.8; DB 4; Length 6103;
Best Local Similarity 52.9%; Pred. No. 8.1e+02;
RESULT 1481
ID ABL34014 standard; DNA; 6182 BP.
DE Human immune system associated gene SEQ ID NO: 1987.
PD WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.9%; Score 29.8; DB 6; Length 6182;
Best Local Similarity 51.1%; Pred. No. 8.1e+02;
RESULT 1482
ID ABL19982 standard; DNA; 6362 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 11419.
PD WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.9%; Score 29.8; DB 4; Length 6362;
Best Local Similarity 56.7%; Pred. No. 8.2e+02;
RESULT 1483
ID ABL32966 standard; DNA; 6381 BP.
DE Human immune system associated gene SEQ ID NO: 939.
PD WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.9%; Score 29.8; DB 6; Length 6381;
Best Local Similarity 49.7%; Pred. No. 8.2e+02;
RESULT 1484
ID ABL34518 standard; DNA; 6381 BP.
DE Human metastasis associated gene SEQ ID NO: 71.
PD WO200177376-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.9%; Score 29.8; DB 6; Length 6381;
Best Local Similarity 49.7%; Pred. No. 8.2e+02;
RESULT 1485
ID ABL70243 standard; DNA; 6381 BP.

DE Chemically treated cell signalling DNA sequence#67.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.9%; Score 29.8; DB 6; Length 6381;
Best Local Similarity 49.7%; Pred. No. 8.2e+02;
RESULT 1486
ID AAG18540 standard; DNA; 8145 BP.
DE Partial galanin receptor (GALR1) gene sequence #2.
PN WO200179237-A2.
PD 25-OCT-2001.
PA (GENA-) GENA/ISSANCE PHARM INC.
Query Match 3.9%; Score 29.8; DB 6; Length 8145;
Best Local Similarity 51.9%; Pred. No. 9.2e+02;
RESULT 1487
ID ABL01872 standard; cDNA; 8542 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 98.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.9%; Score 29.8; DB 4; Length 8542;
Best Local Similarity 56.7%; Pred. No. 9.4e+02;
RESULT 1488
ID AAG45503 standard; DNA; 8996 BP.
DE Chemically pretreated complementary DNA associated with cell cycle #104.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.9%; Score 29.8; DB 4; Length 8996;
Best Local Similarity 51.1%; Pred. No. 9.7e+02;
RESULT 1489
ID ABK28435 standard; DNA; 8996 BP.
DE DNA transcription associated genomic DNA #155.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.9%; Score 29.8; DB 6; Length 8996;
Best Local Similarity 51.1%; Pred. No. 9.7e+02;
RESULT 1490
ID ABL32343 standard; DNA; 11534 BP.
DE Human immune system associated gene SEQ ID NO: 316.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.9%; Score 29.8; DB 6; Length 11534;
Best Local Similarity 43.3%; Pred. No. 1.1e+03;
RESULT 1491
ID ADB54329 standard; DNA; 11787 BP.
DE Pretreated genomic DNA region 253.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.9%; Score 29.8; DB 10; Length 11787;
Best Local Similarity 49.7%; Pred. No. 1.1e+03;
RESULT 1492
ID ABL15354 standard; cDNA; 13075 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 40544.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.9%; Score 29.8; DB 4; Length 13075;
Best Local Similarity 51.9%; Pred. No. 1.2e+03;
RESULT 1493
ID ABL33227 standard; DNA; 13125 BP.
DE Human immune system associated gene SEQ ID NO: 1200.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.9%; Score 29.8; DB 6; Length 13125;
Best Local Similarity 45.2%; Pred. No. 1.2e+03;
RESULT 1494
ID ABL34557 standard; DNA; 13125 BP.
DE Human metastasis associated gene SEQ ID NO: 110.

PN WO200177376-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.9%; Score 29.8; DB 6; Length 13125;
Best Local Similarity 45.2%; Pred. No. 1.2e+03;
RESULT 1495
ID ABL70284 standard; DNA; 13125 BP.
DE Chemically treated cell signalling DNA sequence complementary to#87.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.9%; Score 29.8; DB 6; Length 13125;
Best Local Similarity 45.2%; Pred. No. 1.2e+03;
RESULT 1496
ID ABZ74645 standard; DNA; 17646 BP.
DE Secreted protein gene 381 genomic fragment HE2CA60, SEQ ID NO:1792.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.9%; Score 29.8; DB 8; Length 17646;
Best Local Similarity 58.4%; Pred. No. 1.3e+03;
RESULT 1497
ID ADA98997 standard; DNA; 17646 BP.
DE Human secreted protein-related DNA sequence #590.
PN WO2003004623-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.9%; Score 29.8; DB 8; Length 17646;
Best Local Similarity 58.4%; Pred. No. 1.3e+03;
RESULT 1498
ID ABT17023 standard; DNA; 17646 BP.
DE Human secreted protein-related DNA sequence - SEQ ID NO 377.
PN WO200277188-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.9%; Score 29.8; DB 10; Length 17646;
Best Local Similarity 58.4%; Pred. No. 1.3e+03;
RESULT 1499
ID ABZ68163 standard; DNA; 17646 BP.
DE Human secreted protein encoding genomic DNA SEQ ID NO 1686.
PN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.9%; Score 29.8; DB 10; Length 17646;
Best Local Similarity 58.4%; Pred. No. 1.3e+03;
RESULT 1500
ID ABL32793 standard; DNA; 19087 BP.
DE Human immune system associated gene SEQ ID NO: 766.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.9%; Score 29.8; DB 6; Length 19087;
Best Local Similarity 49.7%; Pred. No. 1.4e+03;

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 24, 2005, 19:07:47 ; Search time 67 Seconds
(without alignments)
8126.333 Million cell up

Title: US-10-063-553-47

Perfect score:

Sequence: 1 ggctcgagcgttctgagcc.....agtagttgaaaaaaaaa 766

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 segs. 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length:

Minimum DB seq length: 9
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

F08C-Processing: Minimum Match 0% Maximum Match 100%

Maximum Match 100%
Listing first 1500 summaries

Database : Tagged Patents NA.*

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6: /cqn2_6/ptodata/1/ina/backfiles1.secd

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	43.8	5.7	1141	4	US-09-806-708B-22
C 2	38.2	5.0	7218	1	US-08-232-463-14
C 3	36.4	4.8	369	4	US-09-107-532A-3165
C 4	35.8	4.7	393	4	US-09-583-110-486
C 5	35.8	4.7	832	4	US-09-621-976-2813
C 6	34.8	4.5	1809	4	US-09-589-733C-5
C 7	34.2	4.5	786431	4	US-09-751-389-3
C 8	34.2	4.4	1284	4	US-09-248-796A-2331
C 9	33.2	4.3	1055	4	US-09-806-708B-23
C 10	33	4.3	609	4	US-09-248-796A-6609
C 11	33	4.3	3103	4	US-09-710-279-3462
C 12	33	4.3	3438	4	US-09-710-279-4241
C 13	33	4.3	3463	4	US-09-710-279-3997
C 14	32.4	4.2	746	3	US-08-998-416-270
C 15	32.2	4.2	414	4	US-09-513-999C-1082
C 16	32.2	4.2	855	4	US-09-552-204A-10
C 17	32	4.2	1441	4	US-09-806-708B-22
C 18	32	4.2	4954	1	US-08-920-813-18
C 19	32	4.2	4954	1	US-08-920-827-18
C 20	32	4.2	4954	1	US-08-921-177-18
C 21	32	4.2	4954	1	US-08-362-577C-18
C 22	32	4.2	4954	2	US-08-920-828-18
C 23	32	4.2	11015	4	US-10-204-708-56
C 24	31.8	4.2	894	4	US-09-976-594-90
C 25	31.8	4.2	640681	4	US-09-790-988-1
C 26	31.6	4.1	855	4	US-09-248-796A-4821
C 27	31.4	4.1	425	4	US-09-621-976-8306

101	30	3.9	1357	4	US-09-461-325-55	Sequence 55, Appl	174	29.2	3.8	2498	4	US-09-620-312D-90	Sequence 90, Appl
102	30	3.9	1357	4	US-10-012-542-55	Sequence 55, Appl	175	29.2	3.8	2920	4	US-09-620-312D-1084	Sequence 1084, Ap
103	30	3.9	1357	4	US-10-115-123-55	Sequence 55, Appl	C 176	29.2	3.8	3522	4	US-09-248-796A-5210	Sequence 5210, Ap
104	30	3.9	1386	4	US-09-539-333D-40	Sequence 40, Appl	C 177	29.2	3.8	75395	4	US-09-984-890-3	Sequence 3, Appl1
105	30	3.9	1902	4	US-09-583-110-1360	Sequence 1360, Ap	C 178	29.2	3.8	75395	4	US-10-274-194-3	Sequence 3, Appl1
106	30	3.9	2007	4	US-09-328-352-2460	Sequence 2460, Ap	C 179	29	3.8	986	4	US-09-270-767-14027	Sequence 14027, A
107	30	3.9	8148	4	US-08-961-527-11	Sequence 11, Appl	C 180	29	3.8	1200	4	US-09-248-796A-4154	Sequence 4154, Ap
108	30	3.9	319608	4	US-09-539-333D-1	Sequence 1, Appl1	C 181	29	3.8	1329	4	US-09-787-083-5	Sequence 5, Appl1
109	30	3.9	319608	4	US-09-679-409-1	Sequence 1, Appl1	C 182	29	3.8	1359	4	US-09-248-796A-6193	Sequence 6193, Ap
110	29.8	3.9	298	4	US-09-313-294A-7544	Sequence 7544, Ap	C 183	29	3.8	1548	4	US-09-248-796A-4161	Sequence 4161, Ap
111	29.8	3.9	567	3	US-09-385-982-427	Sequence 427, App	184	29	3.8	1587	4	US-09-614-221A-202	Sequence 202, App
112	29.8	3.9	698	4	US-09-270-767-9087	Sequence 9087, Ap	185	29	3.8	1609	4	US-09-620-312D-8	Sequence 8, Appl1
113	29.8	3.9	698	4	US-09-270-767-24369	Sequence 24369, A	186	29	3.8	1884	4	US-10-246-658-3	Sequence 3, Appl1
114	29.8	3.9	704	4	US-09-023-655-46	Sequence 46, Appl	C 187	29	3.8	2013	4	US-09-252-858B-1	Sequence 1, Appl1
115	29.8	3.9	1152	1	US-08-315-831A-13	Sequence 13, Appl	C 188	29	3.8	2058	4	US-10-246-658-1	Sequence 1, Appl1
116	29.8	3.9	1152	1	US-08-662-318-13	Sequence 13, Appl	C 189	29	3.8	2652	2	US-08-366-547-1	Sequence 1, Appl1
117	29.8	3.9	1152	5	PCT-US95-12509-13	Sequence 13, Appl	C 190	29	3.8	3001	4	US-09-539-333D-226	Sequence 226, App
118	29.8	3.9	1316	1	US-07-755-461A-12	Sequence 12, Appl	C 191	29	3.8	9048	3	US-08-973-273-4	Sequence 4, Appl1
119	29.8	3.9	1316	1	US-08-315-831A-12	Sequence 12, Appl	C 192	28.8	3.8	250	4	US-09-513-999C-32028	Sequence 32028, A
120	29.8	3.9	1316	1	US-08-662-318-12	Sequence 12, Appl	C 193	28.8	3.8	637	4	US-09-270-767-4501	Sequence 4501, Ap
121	29.8	3.9	1316	5	PCT-US95-12509-12	Sequence 12, Appl	C 194	28.8	3.8	637	4	US-09-270-767-19783	Sequence 19783, A
122	29.8	3.9	1430	4	US-09-016-434-710	Sequence 710, App	C 195	28.8	3.8	802	4	US-09-311-021-87	Sequence 87, Appl
123	29.8	3.9	4608	1	US-07-718-575-11	Sequence 11, Appl	196	28.8	3.8	804	4	US-09-149-476-125	Sequence 125, App
124	29.8	3.9	4608	1	US-08-481-206-11	Sequence 11, Appl	197	28.8	3.8	930	4	US-08-956-171E-813	Sequence 813, App
125	29.8	3.9	4608	2	US-08-486-269A-11	Sequence 11, Appl	198	28.8	3.8	1320	4	US-08-781-986A-813	Sequence 813, App
126	29.8	3.9	112132	4	US-09-741-150-3	Sequence 3, Appl1	C 200	28.8	3.8	1808	1	US-09-351-149-4	Sequence 4, Appl1
127	29.8	3.9	112132	4	US-10-160-187-3	Sequence 3, Appl1	C 201	28.8	3.8	1808	1	US-08-384-828-4	Sequence 4, Appl1
128	29.8	3.9	1830121	4	US-09-557-884-1	Sequence 1, Appl1	C 202	28.8	3.8	1808	3	US-08-895-474-4	Sequence 4, Appl1
129	29.8	3.9	1830121	4	US-09-643-990A-1	Sequence 1, Appl1	C 203	28.8	3.8	1859	3	US-07-861-458C-1	Sequence 1, Appl1
130	29.8	3.9	1830121	4	US-10-329-960-1	Sequence 1, Appl1	C 204	28.8	3.8	1970	4	US-09-311-021-41	Sequence 41, Appl
131	29.6	3.9	400	1	US-08-208-008C-1	Sequence 1, Appl1	C 205	28.8	3.8	2748	3	US-09-199-290-33	Sequence 33, Appl
132	29.6	3.9	500	4	US-09-270-767-9290	Sequence 9290, Ap	C 206	28.8	3.8	2748	3	US-09-821-616-33	Sequence 33, Appl
133	29.6	3.9	500	4	US-09-270-767-24572	Sequence 24572, A	C 207	28.8	3.8	3075	4	US-09-799-451-32	Sequence 32, Appl
134	29.6	3.9	834	4	US-09-328-352-3810	Sequence 3810, Ap	C 208	28.8	3.8	3275	4	US-09-370-838-151	Sequence 151, App
135	29.6	3.9	1449	4	US-09-248-796A-3697	Sequence 3697, Ap	C 209	28.8	3.8	3275	4	US-03-854-133-151	Sequence 151, App
136	29.6	3.9	1565	3	US-08-468-846-1	Sequence 1, Appl1	C 210	28.8	3.8	4407	5	PCT-US93-05701-1	Sequence 1, Appl1
137	29.6	3.9	1565	3	US-08-915-096A-1	Sequence 1, Appl1	C 211	28.8	3.8	5610	4	US-10-204-708-53	Sequence 53, Appl
138	29.6	3.9	1672	4	US-09-023-655-1472	Sequence 1472, Ap	C 212	28.8	3.8	5910	1	US-08-195-814-1	Sequence 1, Appl1
139	29.6	3.9	3288	1	US-08-208-008C-3	Sequence 3, Appl1	C 213	28.8	3.8	605	4	US-08-961-576B-10	Sequence 10, Appl
140	29.6	3.9	5150	3	US-09-068-140A-14	Sequence 14, Appl	C 214	28.6	3.7	506	3	US-08-916-576B-10	Sequence 10, Appl
141	29.6	3.9	9578	4	US-08-961-527-127	Sequence 127, App	C 215	28.6	3.7	570	4	US-09-248-796A-5338	Sequence 5338, Ap
142	29.6	3.9	22846	2	US-08-463-461-3	Sequence 3, Appl1	C 216	28.6	3.7	618	3	US-09-583-982-24	Sequence 24, Appl
143	29.6	3.9	22846	3	US-07-890-609-3	Sequence 3, Appl1	C 217	28.6	3.7	885	4	US-09-583-110-528	Sequence 528, App
144	29.6	3.9	1664976	4	US-08-916-421B-1	Sequence 1, Appl1	C 218	28.6	3.7	1081	4	US-09-016-434-928	Sequence 928, App
145	29.6	3.9	1664976	4	US-09-692-570-1	Sequence 1, Appl1	C 219	28.6	3.7	1173	3	US-08-993-380-3	Sequence 3, Appl1
146	29.6	3.9	1830121	4	US-09-557-884-1	Sequence 1, Appl1	C 220	28.6	3.7	1399	3	US-09-049-698-17	Sequence 17, Appl
147	29.6	3.9	1830121	4	US-09-643-990A-1	Sequence 1, Appl1	C 221	28.6	3.7	1575	3	US-08-639-234-1	Sequence 1, Appl1
148	29.6	3.9	1830121	4	US-10-329-960-1	Sequence 1, Appl1	C 222	28.6	3.7	1575	3	US-09-861-034B-1	Sequence 1, Appl1
149	29.4	3.8	365	4	US-09-621-976-8348	Sequence 8348, Ap	C 223	28.6	3.7	1764	3	US-09-013-881-13	Sequence 13, Appl
150	29.4	3.8	420	4	US-09-134-000C-2341	Sequence 2341, Ap	C 224	28.6	3.7	1764	3	US-09-612-473-13	Sequence 13, Appl
151	29.4	3.8	433	4	US-09-513-999C-24898	Sequence 24898, A	C 225	28.6	3.7	1915	3	US-09-147-915-1	Sequence 1, Appl1
152	29.4	3.8	909	4	US-09-248-796A-3116	Sequence 3116, Ap	C 226	28.6	3.7	1926	1	US-09-270-767-27574	Sequence 27574, A
153	29.4	3.8	1419	4	US-09-248-796A-12098	Sequence 12098, A	C 227	28.6	3.7	2016	1	US-08-294-872-1	Sequence 1, Appl1
154	29.4	3.8	2598	4	US-09-248-796A-3589	Sequence 3589, Ap	C 228	28.6	3.7	2016	5	PCT-US95-09823-1	Sequence 1, Appl1
155	29.4	3.8	4002	2	US-08-540-804-11	Sequence 11, Appl	C 229	28.6	3.7	2661	4	US-09-248-796A-3901	Sequence 3901, Ap
156	29.4	3.8	4002	2	US-08-218-265-11	Sequence 11, Appl	C 230	28.6	3.7	2943	3	US-08-936-165A-201	Sequence 201, App
157	29.4	3.8	4002	3	US-08-521-872-11	Sequence 11, Appl	C 231	28.6	3.7	2943	3	US-09-503-922-2	Sequence 2, Appl1
158	29.4	3.8	4002	3	US-08-590-399-11	Sequence 11, Appl	C 232	28.6	3.7	3018	2	US-08-860-150-6	Sequence 6, Appl1
159	29.4	3.8	4631	4	US-09-799-451-394	Sequence 394, App	C 233	28.6	3.7	3018	3	US-09-338-132-6	Sequence 6, Appl1
160	29.4	3.8	4822	4	US-09-270-767-12784	Sequence 12784, A	C 234	28.6	3.7	3043	3	US-09-049-698-16	Sequence 16, Appl
161	29.4	3.8	29793	3	US-09-302-812-38	Sequence 38, Appl	C 235	28.6	3.7	3181	3	US-09-049-698-18	Sequence 18, Appl
162	29.4	3.8	29793	3	US-09-511-477-38	Sequence 38, Appl	C 236	28.6	3.7	3454	4	US-09-270-767-11909	Sequence 11909, A
163	29.4	3.8	29793	3	US-09-511-507-38	Sequence 38, Appl	C 237	28.6	3.7	4330	3	US-09-310-293-1	Sequence 1, Appl1
164	29.4	3.8	1230025	4	US-09-198-452A-1	Sequence 1, Appl1	C 238	28.6	3.7	4330	3	US-09-579-376-1	Sequence 1, Appl1
165	29.4	3.8	1664976	4	US-08-916-421B-1	Sequence 1, Appl1	C 239	28.6	3.7	4673	5	PCT-US92-00018-1	Sequence 1, Appl1
166	29.4	3.8	1664976	4	US-09-692-570-1	Sequence 1, Appl1	C 240	28.6	3.7	4673	2	US-08-970-269A-32	Sequence 32, Appl
167	29.2	3.8	216	1	US-08-686-878A-34	Sequence 34, Appl	C 241	28.6	3.7	11873	2	US-09-407-562-32	Sequence 32, Appl
168	29.2	3.8	216	3	US-09-175-928-34	Sequence 34, Appl	C 242	28.6	3.7	11873	2	US-08-970-269A-31	Sequence 31, Appl
169	29.2	3.8	456	4	US-09-248-796A-14094	Sequence 14094, A	C 243	28.6	3.7	11878	3	US-09-407-562-31	Sequence 31, Appl
170	29.2	3.8	1011	4	US-09-248-796A-3838	Sequence 3838, Ap	C 244	28.6	3.7	11878	3	US-08-970-269A-28	Sequence 28, Appl
171	29.2	3.8	1477	4	US-09-560-761-27	Sequence 27, Appl	C 245	28.6	3.7	11883	3	US-09-407-562-28	Sequence 28, Appl
172	29.2	3.8	1747	4	US-09-244-805-23	Sequence 23, Appl	C 246	28.6	3.7	11883	3	US-09-407-562-28	Sequence 28, Appl
173	29.2	3.8	2229	4	US-09-774-528-283	Sequence 283, App	C 246	28.6	3.7	11883	3	US-09-407-562-28	Sequence 28, Appl

C 247	28.6	3.7	14051	4	US-08-956-1718-103	Sequence 103, App	C 320	28.2	3.7	2237	4	US-09-148-545-104	Sequence 104, App
C 248	28.6	3.7	14051	4	US-08-781-986A-103	Sequence 103, App	321	28.2	3.7	2577	4	US-09-952-060-1	Sequence 1, Appli
C 249	28.4	3.7	200	4	US-09-688-990-11	Sequence 11, Appl	322	28.2	3.7	2577	4	US-09-952-060-3	Sequence 3, Appli
C 250	28.4	3.7	219	1	US-08-702-080-3	Sequence 3, Appli	323	28.2	3.7	2650	4	US-09-952-060-5	Sequence 5, Appli
C 251	28.4	3.7	219	2	US-08-858-830-3	Sequence 3, Appli	324	28.2	3.7	2650	4	US-09-952-060-7	Sequence 7, Appli
C 252	28.4	3.7	219	2	US-08-858-834-3	Sequence 3, Appli	325	28.2	3.7	2659	4	US-09-148-545-42	Sequence 42, Appl
C 253	28.4	3.7	242	3	US-09-049-698-11	Sequence 11, Appl	326	28.2	3.7	3857	4	US-09-976-594-915	Sequence 915, App
C 254	28.4	3.7	264	4	US-09-556-877-274	Sequence 274, App	327	28.2	3.7	3887	4	US-09-976-594-660	Sequence 660, App
C 255	28.4	3.7	264	4	US-09-620-412C-274	Sequence 274, App	328	28.2	3.7	4053	4	US-09-952-060-34	Sequence 34, Appl
C 256	28.4	3.7	264	4	US-09-598-419-274	Sequence 274, App	329	28.2	3.7	6360	4	US-09-221-017B-835	Sequence 835, App
C 257	28.4	3.7	301	4	US-09-248-796A-12744	Sequence 12744, A	330	28.2	3.7	10564	1	US-08-206-176-5	Sequence 5, Appli
C 258	28.4	3.7	301	4	US-09-270-767-5573	Sequence 5573, A	331	28.2	3.7	10592	1	US-08-680-726A-51	Sequence 51, Appl
C 259	28.4	3.7	301	4	US-09-270-767-20855	Sequence 20855, A	332	28.2	3.7	10592	1	US-08-680-726A-52	Sequence 52, Appl
C 260	28.4	3.7	355	4	US-09-513-999C-1174	Sequence 1174, App	333	28.2	3.7	10592	3	US-09-092-409-51	Sequence 51, Appl
C 261	28.4	3.7	432	4	US-09-248-796A-7360	Sequence 7360, App	334	28.2	3.7	10592	3	US-09-092-409-52	Sequence 52, Appl
C 262	28.4	3.7	469	3	US-09-222-575-128	Sequence 128, App	335	28.2	3.7	15378	3	US-08-785-420-1	Sequence 1, Appli
C 263	28.4	3.7	469	4	US-09-389-681-128	Sequence 128, App	336	28.2	3.7	38519	4	US-09-952-060-28	Sequence 28, Appl
C 264	28.4	3.7	469	4	US-09-620-405B-128	Sequence 128, App	337	28.2	3.7	84495	3	US-09-797-906-3	Sequence 3, Appli
C 265	28.4	3.7	469	4	US-09-339-338-128	Sequence 128, App	338	28.2	3.7	92139	4	US-09-918-686-1	Sequence 1, Appli
C 266	28.4	3.7	469	4	US-09-433-826B-128	Sequence 128, App	339	28.2	3.7	1230025	4	US-09-198-452A-1	Sequence 1, Appli
C 267	28.4	3.7	469	4	US-09-604-287A-128	Sequence 128, App	340	28	3.7	312	3	US-08-746-160-8	Sequence 8, Appli
C 268	28.4	3.7	469	4	US-09-285-480-128	Sequence 128, App	341	28	3.7	312	3	US-08-810-324-5	Sequence 5, Appli
C 269	28.4	3.7	469	4	US-09-834-759-128	Sequence 128, App	342	28	3.7	360	3	US-08-746-160-2	Sequence 2, Appli
C 270	28.4	3.7	469	4	US-09-590-751A-128	Sequence 128, App	343	28	3.7	360	3	US-08-810-324-2	Sequence 2, Appli
C 271	28.4	3.7	526	4	US-09-621-976-3217	Sequence 3217, App	344	28	3.7	381	2	US-08-808-277A-2	Sequence 2, Appli
C 272	28.4	3.7	738	4	US-09-248-796A-931	Sequence 931, App	345	28	3.7	387	2	US-08-480-774A-3	Sequence 3, Appli
C 273	28.4	3.7	855	4	US-09-248-796A-10854	Sequence 10854, A	346	28	3.7	389	2	US-08-808-277A-8	Sequence 8, Appli
C 274	28.4	3.7	1128	1	US-08-381-280-9	Sequence 4, Appli	347	28	3.7	438	4	US-09-513-999C-27526	Sequence 27526, A
C 275	28.4	3.7	1128	1	US-08-381-280-9	Sequence 9, Appli	348	28	3.7	608	3	US-09-385-982-36	Sequence 36, Appl
C 276	28.4	3.7	1128	1	US-08-381-280-18	Sequence 18, Appl	349	28	3.7	870	3	US-09-134-001C-80	Sequence 80, Appl
C 277	28.4	3.7	1128	2	US-08-445-533-4	Sequence 9, Appli	350	28	3.7	961	4	US-09-671-317-5	Sequence 5, Appli
C 278	28.4	3.7	1128	2	US-08-445-533-9	Sequence 9, Appli	351	28	3.7	1134	4	US-10-101-464A-323	Sequence 323, App
C 279	28.4	3.7	1128	2	US-08-445-533-18	Sequence 18, Appl	352	28	3.7	1227	4	US-09-248-796A-7521	Sequence 7521, Ap
C 280	28.4	3.7	1128	3	US-09-052-085-4	Sequence 4, Appli	353	28	3.7	1420	4	US-09-690-942-11	Sequence 11, Appl
C 281	28.4	3.7	1128	3	US-09-052-085-9	Sequence 9, Appli	354	28	3.7	1422	3	US-08-387-117-8	Sequence 8, Appli
C 282	28.4	3.7	1128	3	US-09-052-085-18	Sequence 18, Appl	355	28	3.7	1482	4	US-09-252-991A-11453	Sequence 11453, A
C 283	28.4	3.7	1188	1	US-08-048-700-1	Sequence 1, Appli	356	28	3.7	1905	3	US-08-387-117-7	Sequence 7, Appli
C 284	28.4	3.7	1188	3	US-08-839-711-5	Sequence 5, Appli	357	28	3.7	2277	1	US-08-676-967-2	Sequence 2, Appli
C 285	28.4	3.7	1226	1	US-08-374-686-4	Sequence 4, Appli	358	28	3.7	2277	1	US-08-676-974-2	Sequence 2, Appli
C 286	28.4	3.7	1296	4	US-09-134-000C-1947	Sequence 1947, Ap	359	28	3.7	2277	2	US-09-098-487-2	Sequence 2, Appli
C 287	28.4	3.7	1349	1	US-08-374-686-1	Sequence 1, Appli	360	28	3.7	5102	4	US-09-023-655-1426	Sequence 1426, Ap
C 288	28.4	3.7	1470	4	US-09-016-434-1203	Sequence 1203, Ap	361	28	3.7	5102	4	US-09-919-497-8	Sequence 8, Appli
C 289	28.4	3.7	1588	3	US-08-858-207A-58	Sequence 58, Appl	362	28	3.7	7141	4	US-09-631-594-73	Sequence 73, Appl
C 290	28.4	3.7	1716	4	US-09-710-279-117	Sequence 117, App	363	28	3.7	11831	4	US-08-961-527-65	Sequence 65, Appl
C 291	28.4	3.7	1722	3	US-09-134-001C-2189	Sequence 2189, Ap	364	28	3.7	19446	4	US-08-961-527-51	Sequence 51, Appl
C 292	28.4	3.7	1786	4	US-09-976-594-274	Sequence 274, App	365	28	3.7	640681	4	US-09-790-988-1	Sequence 1, Appli
C 293	28.4	3.7	1873	3	US-08-910-864-13	Sequence 13, Appl	366	27.8	3.6	357	4	US-09-513-999C-19160	Sequence 19160, A
C 294	28.4	3.7	2733	4	US-09-107-532A-2699	Sequence 2699, Ap	367	27.8	3.6	546	4	US-09-543-681A-1765	Sequence 1765, Ap
C 295	28.4	3.7	3164	4	US-09-710-279-3828	Sequence 3828, Ap	368	27.8	3.6	573	4	US-09-248-796A-5065	Sequence 5065, Ap
C 296	28.4	3.7	3234	4	US-09-710-279-3853	Sequence 3853, Ap	369	27.8	3.6	702	4	US-09-472-087-41	Sequence 41, Appl
C 297	28.4	3.7	3475	4	US-09-710-279-4032	Sequence 4032, Ap	370	27.8	3.6	702	4	US-09-472-087-58	Sequence 58, Appl
C 298	28.4	3.7	4301	3	US-08-121-446-3	Sequence 3, Appli	371	27.8	3.6	873	4	US-09-248-796A-298	Sequence 298, App
C 299	28.4	3.7	5852	1	US-07-867-106-2	Sequence 2, Appli	372	27.8	3.6	954	4	US-09-248-796A-392	Sequence 392, App
C 300	28.4	3.7	50000	3	US-09-146-053-3	Sequence 3, Appli	373	27.8	3.6	988	4	US-09-774-528-432	Sequence 432, App
C 301	28.2	3.7	391	2	US-08-808-277A-10	Sequence 10, Appl	374	27.8	3.6	1002	4	US-09-134-000C-2083	Sequence 2083, Ap
C 302	28.2	3.7	504	3	US-08-965-030B-14	Sequence 14, Appl	375	27.8	3.6	1241	4	US-09-737-698B-25	Sequence 25, Appl
C 303	28.2	3.7	546	4	US-09-248-796A-13542	Sequence 13542, A	376	27.8	3.6	1241	4	US-09-737-626A-25	Sequence 25, Appl
C 304	28.2	3.7	782	4	US-09-780-717-31	Sequence 31, Appl	377	27.8	3.6	1290	4	US-10-251-503-1	Sequence 1, Appli
C 305	28.2	3.7	789	6	5219739-8	Patent No. 5219739	378	27.8	3.6	1533	3	US-09-002-285-89	Sequence 89, Appl
C 306	28.2	3.7	975	4	US-09-248-796A-5867	Sequence 5867, Ap	379	27.8	3.6	1533	4	US-09-589-477-89	Sequence 89, Appl
C 307	28.2	3.7	1014	4	US-09-325-932A-15	Sequence 15, Appl	380	27.8	3.6	1533	4	US-10-099-285A-89	Sequence 89, Appl
C 308	28.2	3.7	1276	4	US-09-673-395A-108	Sequence 108, App	381	27.8	3.6	1756	2	US-08-879-260-3	Sequence 3, Appli
C 309	28.2	3.7	1278	4	US-09-248-796A-1321	Sequence 1321, App	382	27.8	3.6	1788	4	US-09-583-110-1283	Sequence 1283, Ap
C 310	28.2	3.7	1434	4	US-09-673-395A-113	Sequence 113, App	383	27.8	3.6	1811	3	US-09-231-529-5	Sequence 5, Appli
C 311	28.2	3.7	1434	4	US-09-673-395A-551	Sequence 551, App	384	27.8	3.6	1811	3	US-08-977-816-5	Sequence 5, Appli
C 312	28.2	3.7	1452	4	US-09-248-796A-6115	Sequence 6115, Ap	385	27.8	3.6	1822	2	US-08-757-046A-2	Sequence 2, Appli
C 313	28.2	3.7	1664	1	US-08-250-740-34	Sequence 34, Appl	386	27.8	3.6	1822	3	US-09-447-208-2	Sequence 2, Appli
C 314	28.2	3.7	1664	1	US-07-695-472B-3	Sequence 3, Appli	387	27.8	3.6	1822	3	US-09-135-988-2	Sequence 2, Appli
C 315	28.2	3.7	1664	4	US-09-106-375-3	Sequence 3, Appli	388	27.8	3.6	1822	3	US-09-277-716-2	Sequence 2, Appli
C 316	28.2	3.7	1675	4	US-09-854-133-395	Sequence 395, App	389	27.8	3.6	1822	3	US-08-597-274A-2	Sequence 2, Appli
C 317	28.2	3.7	1736	4	US-09-620-312B-540	Sequence 540, App	390	27.8	3.6	1822	4	US-08-908-909-2	Sequence 2, Appli
C 318	28.2	3.7	1865	4	US-09-620-312D-539	Sequence 539, App	391	27.8	3.6	1822	4	US-09-609-161B-2	Sequence 2, Appli
C 319	28.2	3.7	2000	4	US-09-705-267A-19	Sequence 19, Appl	392	27.8	3.6	1822	4	US-08-990-103-2	Sequence 2, Appli

393	27.8	3.6	1822	4	US-09-746-485A-2	Sequence 2, Appli	C 466	27.6	3.6	4210	4	US-09-710-279-3761	Sequence 3761, Ap
394	27.8	3.6	1822	4	US-10-126-139-2	Sequence 2, Appli	C 467	27.6	3.6	5055	3	US-09-242-632A-13	Sequence 13, Appli
395	27.8	3.6	1822	4	US-10-126-798-2	Sequence 2, Appli	C 468	27.6	3.6	5652	4	US-09-601-198-75	Sequence 75, Appli
396	27.8	3.6	1822	4	US-10-126-777-2	Sequence 2, Appli	C 469	27.6	3.6	6156	4	US-09-392-812A-3	Sequence 3, Appli
397	27.8	3.6	2268	4	US-09-642-034-4	Sequence 4, Appli	C 470	27.6	3.6	6527	4	US-09-492-308A-3	Sequence 3, Appli
398	27.8	3.6	2290	6	5312912-1	Patent No. 5312912	C 471	27.6	3.6	6854	4	US-08-961-527-200	Sequence 200, App
399	27.8	3.6	2364	4	US-09-307-106-53	Sequence 53, Appli	C 472	27.6	3.6	8961	4	US-10-204-708-79	Sequence 79, Appli
400	27.8	3.6	2366	4	US-09-002-285-99	Sequence 99, Appli	C 473	27.6	3.6	16995	4	US-08-961-527-82	Sequence 82, Appli
401	27.8	3.6	2366	4	US-09-002-285-99	Sequence 99, Appli	C 474	27.6	3.6	24358	4	US-09-392-812A-1	Sequence 1, Appli
402	27.8	3.6	2366	4	US-10-099-285A-99	Sequence 99, Appli	C 475	27.6	3.6	37950	3	US-09-338-907-183	Sequence 183, App
403	27.8	3.6	2369	3	US-09-002-285-93	Sequence 93, Appli	C 476	27.6	3.6	37950	3	US-09-218-207-183	Sequence 183, App
404	27.8	3.6	2369	4	US-09-589-477-93	Sequence 93, Appli	C 477	27.6	3.6	137000	4	US-10-172-911-11	Sequence 11, Appli
405	27.8	3.6	2369	4	US-09-002-285-93	Sequence 93, Appli	C 478	27.6	3.6	395	4	US-09-621-976-8495	Sequence 8495, Ap
406	27.8	3.6	2375	3	US-10-099-285A-93	Sequence 93, Appli	C 479	27.4	3.6	432	4	US-09-248-796A-7188	Sequence 7188, Ap
407	27.8	3.6	2375	3	US-09-002-285-85	Sequence 85, Appli	C 480	27.4	3.6	453	4	US-09-270-767-17683	Sequence 17683, A
408	27.8	3.6	2375	4	US-09-589-477-85	Sequence 85, Appli	C 481	27.4	3.6	453	4	US-09-270-767-17683	Sequence 17683, A
409	27.8	3.6	2375	4	US-09-589-477-85	Sequence 85, Appli	C 482	27.4	3.6	453	4	US-09-270-767-17683	Sequence 17683, A
410	27.8	3.6	2375	4	US-10-099-285A-103	Sequence 103, App	C 483	27.4	3.6	609	4	US-09-248-796A-10616	Sequence 10616, A
411	27.8	3.6	2375	4	US-09-642-034-1	Sequence 1, Appli	C 484	27.4	3.6	631	4	US-09-248-796A-5629	Sequence 5629, Ap
412	27.8	3.6	7766	4	US-09-125-619-3	Sequence 3, Appli	C 485	27.4	3.6	643	4	US-09-270-767-10068	Sequence 10068, A
413	27.8	3.6	7766	4	US-10-222-566-3	Sequence 3, Appli	C 486	27.4	3.6	741	4	US-09-385-982-16	Sequence 16, Appli
414	27.8	3.6	7766	4	US-10-143-024A-3	Sequence 3, Appli	C 487	27.4	3.6	987	4	US-09-134-000C-780	Sequence 780, App
415	27.8	3.6	10970	3	US-08-716-351A-5	Sequence 5, Appli	C 488	27.4	3.6	1041	4	US-09-509-712B-105	Sequence 105, App
416	27.8	3.6	14231	4	US-08-961-527-81	Sequence 81, Appli	C 489	27.4	3.6	1329	4	US-09-540-236-1282	Sequence 1282, Ap
417	27.8	3.6	15225	2	US-08-892-403A-2	Sequence 2, Appli	C 490	27.4	3.6	1329	4	US-09-787-083-1	Sequence 1, Appli
418	27.8	3.6	15225	2	US-09-291-894-2	Sequence 2, Appli	C 491	27.4	3.6	1329	4	US-09-787-083-1	Sequence 1, Appli
419	27.8	3.6	15225	2	US-09-291-894-2	Sequence 2, Appli	C 492	27.4	3.6	1329	4	US-09-787-083-1	Sequence 1, Appli
420	27.8	3.6	16995	4	US-08-961-527-82	Sequence 82, Appli	C 493	27.4	3.6	1455	4	US-09-270-767-30203	Sequence 39, Appli
421	27.8	3.6	38844	3	US-09-734-675-3	Sequence 3, Appli	C 494	27.4	3.6	1531	3	US-09-347-878-39	Sequence 7, Appli
422	27.8	3.6	65042	4	US-09-784-316-3	Sequence 3, Appli	C 495	27.4	3.6	1758	4	US-09-462-951B-2	Sequence 2, Appli
423	27.8	3.6	65042	4	US-10-229-124-3	Sequence 3, Appli	C 496	27.4	3.6	2017	4	US-09-270-767-12457	Sequence 2, Appli
424	27.8	3.6	90050	3	US-09-245-041-5	Sequence 5, Appli	C 497	27.4	3.6	2187	4	US-09-270-767-14103	Sequence 14103, A
425	27.8	3.6	90050	4	US-09-358-055B-5	Sequence 5, Appli	C 498	27.4	3.6	2592	4	US-09-620-312D-301	Sequence 301, App
426	27.8	3.6	90050	4	US-09-893-238-5	Sequence 5, Appli	C 499	27.4	3.6	5527	3	US-08-913-374-1	Sequence 1, Appli
427	27.8	3.6	246240	2	US-08-724-394A-20	Sequence 20, Appli	C 500	27.4	3.6	5527	3	US-09-696-115B-1	Sequence 1, Appli
428	27.8	3.6	246240	2	US-08-724-394A-21	Sequence 21, Appli	C 501	27.4	3.6	5733	2	US-08-473-553A-1	Sequence 1, Appli
429	27.8	3.6	246240	2	US-08-724-394A-22	Sequence 22, Appli	C 502	27.4	3.6	6669	4	US-10-204-708-6	Sequence 6, Appli
430	27.6	3.6	187	4	US-09-621-976-13418	Sequence 13418, A	C 503	27.4	3.6	7304	4	US-10-204-708-6	Sequence 6, Appli
431	27.6	3.6	261	4	US-09-248-796A-11472	Sequence 11472, A	C 504	27.4	3.6	7585	4	US-09-418-710-22	Sequence 22, Appli
432	27.6	3.6	273	4	US-09-270-767-6188	Sequence 6188, Ap	C 505	27.4	3.6	7585	4	US-09-839-479-22	Sequence 22, Appli
433	27.6	3.6	273	4	US-09-270-767-6188	Sequence 6188, Ap	C 506	27.4	3.6	7995	4	US-09-821-726A-11	Sequence 11, Appli
434	27.6	3.6	291	4	US-09-583-110-928	Sequence 21470, A	C 507	27.4	3.6	8959	1	US-08-920-821-1	Sequence 1, Appli
435	27.6	3.6	302	4	US-09-583-110-928	Sequence 928, App	C 508	27.4	3.6	8959	1	US-08-920-827-1	Sequence 1, Appli
436	27.6	3.6	324	4	US-09-513-999C-2028	Sequence 2028, Ap	C 509	27.4	3.6	8959	1	US-08-921-177-1	Sequence 1, Appli
437	27.6	3.6	339	4	US-09-248-796A-5971	Sequence 5971, Ap	C 510	27.4	3.6	8959	2	US-08-362-577C-1	Sequence 1, Appli
438	27.6	3.6	345	4	US-09-248-796A-7481	Sequence 7481, Ap	C 511	27.4	3.6	8959	3	US-08-920-828-1	Sequence 1, Appli
439	27.6	3.6	490	4	US-09-430-470-5	Sequence 5, Appli	C 512	27.4	3.6	9060	2	US-08-378-313-20	Sequence 20, Appli
440	27.6	3.6	493	4	US-09-430-470-9	Sequence 9, Appli	C 513	27.4	3.6	12127	4	US-08-961-527-148	Sequence 148, App
441	27.6	3.6	496	4	US-09-430-470-7	Sequence 7, Appli	C 514	27.4	3.6	13059	4	US-08-956-171B-220	Sequence 220, App
442	27.6	3.6	499	4	US-09-430-470-3	Sequence 3, Appli	C 515	27.4	3.6	13059	4	US-08-781-986A-220	Sequence 220, App
443	27.6	3.6	618	4	US-09-134-000C-709	Sequence 709, App	C 516	27.4	3.6	15572	4	US-09-424-783-1	Sequence 1, Appli
444	27.6	3.6	618	4	US-09-134-000C-2782	Sequence 2782, Ap	C 517	27.4	3.6	92407	4	US-09-596-002-36	Sequence 36, Appli
445	27.6	3.6	836	4	US-08-961-309-63	Sequence 63, Appli	C 518	27.4	3.6	148567	4	US-09-801-876B-3	Sequence 3, Appli
446	27.6	3.6	945	4	US-09-583-110-392	Sequence 332, App	C 519	27.4	3.6	148567	4	US-10-254-869-3	Sequence 3, Appli
447	27.6	3.6	1014	4	US-09-107-532A-2344	Sequence 2344, Ap	C 520	27.4	3.6	4403765	3	US-09-103-840A-2	Sequence 2, Appli
448	27.6	3.6	1362	4	US-09-543-661A-3528	Sequence 3528, Ap	C 521	27.4	3.6	4411529	3	US-09-103-840A-1	Sequence 1, Appli
449	27.6	3.6	1449	4	US-09-634-238-36	Sequence 36, Appli	C 522	27.2	3.6	270	4	US-09-621-976-16092	Sequence 16092, A
450	27.6	3.6	1632	4	US-09-248-796A-6825	Sequence 6825, Ap	C 523	27.2	3.6	275	4	US-09-513-999C-23513	Sequence 23513, A
451	27.6	3.6	1660	4	US-09-270-767-158	Sequence 158, App	C 524	27.2	3.6	282	4	US-09-248-796A-9539	Sequence 9539, Ap
452	27.6	3.6	1660	4	US-09-270-767-158	Sequence 158, App	C 525	27.2	3.6	285	4	US-09-313-294A-5273	Sequence 5273, Ap
453	27.6	3.6	1664	4	US-09-270-767-15440	Sequence 15440, A	C 526	27.2	3.6	516	4	US-09-248-796A-10405	Sequence 10405, A
454	27.6	3.6	1664	4	US-09-438-917-5	Sequence 5, Appli	C 527	27.2	3.6	519	4	US-09-248-796A-5916	Sequence 5916, Ap
455	27.6	3.6	1827	3	US-09-315-793-21	Sequence 21, Appli	C 528	27.2	3.6	655	4	US-09-288-143-20	Sequence 20, Appli
456	27.6	3.6	2160	2	US-08-840-236-2	Sequence 2, Appli	C 529	27.2	3.6	687	4	US-09-328-352-1650	Sequence 1650, Ap
457	27.6	3.6	2160	2	US-08-840-236-5	Sequence 5, Appli	C 530	27.2	3.6	932	4	US-09-370-767-14999	Sequence 14999, A
458	27.6	3.6	2160	2	US-08-505-448A-2	Sequence 2, Appli	C 531	27.2	3.6	951	4	US-09-107-532A-940	Sequence 940, App
459	27.6	3.6	2169	4	US-09-434-408-3	Sequence 3, Appli	C 532	27.2	3.6	975	4	US-09-710-279-2673	Sequence 2673, Ap
460	27.6	3.6	2375	3	US-09-002-285-83	Sequence 83, Appli	C 533	27.2	3.6	1188	4	US-09-248-796A-6299	Sequence 6299, Ap
461	27.6	3.6	2375	4	US-09-589-477-83	Sequence 83, Appli	C 534	27.2	3.6	1287	3	US-09-134-001C-2042	Sequence 2042, Ap
462	27.6	3.6	2375	4	US-09-589-477-83	Sequence 83, Appli	C 535	27.2	3.6	1557	3	US-09-710-279-505	Sequence 505, App
463	27.6	3.6	2906	3	US-09-453-702B-186	Sequence 186, App	C 536	27.2	3.6	1584	3	US-09-134-001C-1628	Sequence 1628, Ap
464	27.6	3.6	3467	3	US-09-298-924-3	Sequence 3, Appli	C 537	27.2	3.6	1700	3	US-08-897-340-4	Sequence 4, Appli
465	27.6	3.6	3592	2	US-08-469-537A-100	Sequence 100, App	C 538	27.2	3.6	1722	4	US-09-252-329-4	Sequence 4, Appli
												US-09-248-796A-1650	Sequence 1650, Ap

C 539	27.2	3.6	1730	4	US-09-675-018B-5	Sequence 5, Appli	612	27	3.5	1853	4	US-09-585-166A-369	Sequence 369, App
C 540	27.2	3.6	1854	4	US-09-620-312D-793	Sequence 793, App	613	27	3.5	1853	4	US-09-429-755-295	Sequence 295, App
541	27.2	3.6	1923	4	US-09-149-476-192	Sequence 192, App	614	27	3.5	1853	4	US-09-679-426-369	Sequence 369, App
542	27.2	3.6	1988	4	US-09-643-597-173	Sequence 173, App	C 615	27	3.5	2046	4	US-09-543-681A-1281	Sequence 1281, App
543	27.2	3.6	1988	4	US-09-480-884A-173	Sequence 173, App	C 616	27	3.5	2079	4	US-09-540-236-830	Sequence 830, App
544	27.2	3.6	1988	4	US-09-542-615A-173	Sequence 173, App	C 617	27	3.5	2184	3	US-09-439-313-370	Sequence 370, App
545	27.2	3.6	1988	4	US-09-606-421B-173	Sequence 173, App	C 618	27	3.5	2184	3	US-09-062-451-296	Sequence 296, App
546	27.2	3.6	1988	4	US-09-466-396A-173	Sequence 173, App	C 619	27	3.5	2184	3	US-09-352-616A-370	Sequence 370, App
547	27.2	3.6	1988	4	US-09-476-496A-173	Sequence 173, App	C 620	27	3.5	2184	4	US-09-289-198-296	Sequence 296, App
548	27.2	3.6	1988	4	US-09-630-940B-173	Sequence 173, App	C 621	27	3.5	2184	4	US-09-636-215-370	Sequence 370, App
C 549	27.2	3.6	2049	4	US-09-134-000C-1883	Sequence 1883, Ap	C 622	27	3.5	2184	4	US-09-685-166A-370	Sequence 370, App
C 550	27.2	3.6	2084	4	US-09-197-970B-2	Sequence 2, Appli	C 623	27	3.5	2184	4	US-09-429-755-296	Sequence 296, App
C 551	27.2	3.6	2086	4	US-09-270-767-5329	Sequence 5329, Ap	C 624	27	3.5	2184	4	US-09-679-426-370	Sequence 370, App
C 552	27.2	3.6	2086	4	US-09-270-767-20611	Sequence 20611, A	C 625	27	3.5	2359	2	US-08-961-527-243	Sequence 243, App
C 553	27.2	3.6	2566	4	US-09-197-970B-1	Sequence 1, Appli	C 626	27	3.5	2682	2	US-08-867-941-7	Sequence 7, Appli
C 554	27.2	3.6	3124	4	US-09-710-279-4128	Sequence 4128, Ap	C 627	27	3.5	2682	2	US-09-074-658-7	Sequence 7, Appli
C 555	27.2	3.6	3202	4	US-09-710-279-3386	Sequence 3386, Ap	C 628	27	3.5	2694	2	US-08-867-941-2	Sequence 2, Appli
C 556	27.2	3.6	3498	4	US-09-200-650B-8	Sequence 8, Appli	C 629	27	3.5	2694	3	US-09-074-658-2	Sequence 2, Appli
C 557	27.2	3.6	3675	4	US-09-107-532A-2566	Sequence 2566, Ap	C 630	27	3.5	2985	4	US-09-248-796A-1170	Sequence 1170, Ap
C 558	27.2	3.6	3842	3	US-09-115-954-7	Sequence 7, Appli	C 631	27	3.5	3043	4	US-09-710-279-3576	Sequence 3576, Ap
C 559	27.2	3.6	3912	3	US-09-115-954-1	Sequence 1, Appli	C 632	27	3.5	3135	4	US-09-107-532A-1575	Sequence 1575, Ap
C 560	27.2	3.6	4100	4	US-09-620-312D-81	Sequence 81, Appl	C 633	27	3.5	3135	4	US-09-620-312D-105	Sequence 105, App
C 561	27.2	3.6	4130	4	US-09-710-279-4126	Sequence 4126, Ap	C 634	27	3.5	3546	3	US-09-118-442-14	Sequence 14, Appl
C 562	27.2	3.6	4260	4	US-09-635-132-18	Sequence 18, Appl	C 635	27	3.5	3546	3	US-09-118-442-15	Sequence 15, Appl
C 563	27.2	3.6	4599	1	US-08-431-080-27	Sequence 27, Appl	C 636	27	3.5	3546	3	US-09-677-064-14	Sequence 14, Appl
C 564	27.2	3.6	4599	2	US-08-938-534-27	Sequence 27, Appl	C 637	27	3.5	3546	3	US-09-677-064-15	Sequence 15, Appl
C 565	27.2	3.6	4599	3	US-09-345-294-27	Sequence 27, Appl	C 638	27	3.5	3600	3	US-08-894-731-1	Sequence 1, Appli
C 566	27.2	3.6	5538	2	US-08-231-193A-55	Sequence 55, Appl	C 639	27	3.5	3636	3	US-09-090-535-5	Sequence 5, Appli
C 567	27.2	3.6	5538	2	US-08-486-273A-55	Sequence 55, Appl	C 640	27	3.5	3636	3	US-09-090-535-6	Sequence 6, Appli
C 568	27.2	3.6	5538	3	US-08-940-086A-55	Sequence 55, Appl	C 641	27	3.5	3636	3	US-09-090-535-7	Sequence 7, Appli
C 569	27.2	3.6	5538	3	US-08-940-035A-55	Sequence 55, Appl	C 642	27	3.5	3636	3	US-09-090-535-8	Sequence 8, Appli
C 570	27.2	3.6	5538	3	US-08-935-105A-55	Sequence 55, Appl	C 643	27	3.5	3997	4	US-09-270-767-28607	Sequence 28607, A
C 571	27.2	3.6	5538	4	US-09-648-797-55	Sequence 55, Appl	C 644	27	3.5	4689	4	US-09-895-652A-10	Sequence 10, Appl
C 572	27.2	3.6	5538	4	US-09-386-123-55	Sequence 55, Appl	C 645	27	3.5	4770	4	US-09-543-681A-826	Sequence 826, App
C 573	27.2	3.6	5892	4	US-09-583-110-2582	Sequence 2582, Ap	C 646	27	3.5	5362	2	US-08-853-310-3	Sequence 3, Appli
C 574	27.2	3.6	5915	4	US-10-204-708-78	Sequence 78, Appl	C 647	27	3.5	5421	4	US-09-814-915A-66	Sequence 66, Appli
C 575	27.2	3.6	5983	3	US-08-264-578-1	Sequence 1, Appli	C 648	27	3.5	7641	2	US-08-867-941-6	Sequence 6, Appli
C 576	27.2	3.6	20303	1	US-08-370-975B-6	Sequence 6, Appli	C 649	27	3.5	7641	3	US-09-074-658-6	Sequence 6, Appli
C 577	27.2	3.6	25464	4	US-09-326-480A-4	Sequence 4, Appli	C 650	27	3.5	7650	2	US-08-867-941-1	Sequence 1, Appli
C 578	27.2	3.6	26764	1	US-08-370-975B-1	Sequence 1, Appli	C 651	27	3.5	7850	3	US-09-074-658-1	Sequence 1, Appli
C 579	27.2	3.6	112132	4	US-09-741-150-3	Sequence 3, Appli	C 652	27	3.5	11049	4	US-10-204-708-22	Sequence 22, Appl
C 580	27.2	3.6	112132	4	US-10-160-187-3	Sequence 3, Appli	C 653	27	3.5	19011	1	US-08-310-356-36	Sequence 36, Appl
C 581	27.2	3.6	168575	4	US-09-426-290-1	Sequence 1, Appli	C 654	27	3.5	19557	5	PCT-US32-06300-1	Sequence 1, Appli
C 582	27.2	3.6	169998	4	US-09-676-610B-24	Sequence 24, Appl	C 655	27	3.5	38564	4	US-09-734-673-3	Sequence 3, Appli
C 583	27.2	3.6	197496	4	US-09-877-177A-10	Sequence 10, Appl	C 656	27	3.5	53332	4	US-09-801-861-3	Sequence 3, Appli
C 584	27.2	3.6	202001	4	US-09-734-674-3	Sequence 3, Appli	C 657	27	3.5	53332	4	US-10-224-562-3	Sequence 3, Appli
C 585	27.2	3.6	786431	4	US-09-751-389-3	Sequence 3, Appli	C 658	27	3.5	55827	4	US-09-813-133A-3	Sequence 3, Appli
C 586	27	3.5	323	4	US-09-270-767-7062	Sequence 7062, Ap	C 659	27	3.5	319608	4	US-09-539-333D-1	Sequence 1, Appli
C 587	27	3.5	323	4	US-09-270-767-22344	Sequence 22344, A	C 660	27	3.5	392000	4	US-10-027-983-11	Sequence 11, Appl
C 588	27	3.5	385	4	US-09-621-976-9028	Sequence 9028, Ap	C 661	26.8	3.5	192	4	US-09-248-796A-8980	Sequence 8980, Ap
C 589	27	3.5	402	4	US-09-270-767-8087	Sequence 8087, Ap	C 662	26.8	3.5	296	4	US-09-023-655-349	Sequence 349, App
C 590	27	3.5	402	4	US-09-270-767-23369	Sequence 23369, A	C 663	26.8	3.5	303	4	US-09-513-999C-2162	Sequence 2162, Ap
C 591	27	3.5	438	4	US-09-134-000C-607	Sequence 607, App	C 664	26.8	3.5	330	4	US-09-513-999C-1356	Sequence 1356, Ap
C 592	27	3.5	546	4	US-09-248-796A-4484	Sequence 4484, Ap	C 665	26.8	3.5	474	4	US-09-621-976-18033	Sequence 18033, A
C 593	27	3.5	574	4	US-09-221-017B-370	Sequence 370, App	C 666	26.8	3.5	478	4	US-09-621-976-18425	Sequence 18425, A
C 594	27	3.5	615	4	US-09-854-133-607	Sequence 607, App	C 667	26.8	3.5	505	4	US-09-621-976-15639	Sequence 15639, A
C 595	27	3.5	885	4	US-09-583-110-1634	Sequence 1634, Ap	C 668	26.8	3.5	519	4	US-09-107-532A-2906	Sequence 2906, Ap
C 596	27	3.5	1086	4	US-09-543-681A-2888	Sequence 2888, Ap	C 669	26.8	3.5	581	4	US-09-370-767-7439	Sequence 7439, Ap
C 597	27	3.5	1283	1	US-07-985-970A-7	Sequence 17, Appl	C 670	26.8	3.5	581	4	US-09-270-767-22721	Sequence 22721, A
C 598	27	3.5	1283	1	US-08-298-687A-17	Sequence 17, Appl	C 671	26.8	3.5	585	4	US-09-543-681A-2563	Sequence 2563, Ap
C 599	27	3.5	1283	1	US-08-530-797-18	Sequence 18, Appl	C 672	26.8	3.5	747	4	US-09-248-796A-4877	Sequence 4877, Ap
C 600	27	3.5	1283	1	US-08-298-829-17	Sequence 17, Appl	C 673	26.8	3.5	804	3	US-09-134-000C-387	Sequence 387, App
C 601	27	3.5	1283	2	US-08-787-335-18	Sequence 18, Appl	C 674	26.8	3.5	804	4	US-09-134-000C-2801	Sequence 2801, Ap
C 602	27	3.5	1338	4	US-09-870-472A-7	Sequence 7, Appli	C 675	26.8	3.5	808	4	US-09-270-767-7839	Sequence 7839, Ap
C 603	27	3.5	1462	4	US-09-672-749-12	Sequence 12, Appl	C 676	26.8	3.5	808	4	US-09-270-767-23121	Sequence 23121, A
C 604	27	3.5	1569	2	US-08-743-637B-176	Sequence 176, App	C 677	26.8	3.5	847	4	US-09-270-767-4112	Sequence 4112, Ap
C 605	27	3.5	1569	3	US-08-526-840B-176	Sequence 176, App	C 678	26.8	3.5	847	4	US-09-270-767-11609	Sequence 11609, A
C 606	27	3.5	1686	4	US-09-356-806-41	Sequence 41, Appl	C 679	26.8	3.5	887	4	US-09-270-767-19394	Sequence 19394, A
C 607	27	3.5	1853	3	US-09-439-313-369	Sequence 369, App	C 680	26.8	3.5	909	3	US-08-839-711-2	Sequence 2, Appli
C 608	27	3.5	1853	3	US-09-062-451-295	Sequence 295, App	C 681	26.8	3.5	984	3	US-09-277-565-12	Sequence 12, Appl
C 609	27	3.5	1853	3	US-09-352-616A-369	Sequence 369, App	C 682	26.8	3.5	1308	4	US-09-710-279-3185	Sequence 3185, Ap
C 610	27	3.5	1853	4	US-09-289-198-295	Sequence 295, App	C 683	26.8	3.5	1320	4	US-09-248-796A-1863	Sequence 1865, Ap
C 611	27	3.5	1853	4	US-09-636-215-369	Sequence 369, App	C 684	26.8	3.5	1392	3	US-09-134-000C-1323	Sequence 1323, Ap

C 685	26.8	3.5	1407	4	US-09-248-796A-4441	Sequence 4441, Ap	758	26.6	3.5	445	4	US-09-270-767-4196	Sequence 4196, Ap
C 686	26.8	3.5	1551	4	US-09-328-352-1513	Sequence 1513, Ap	759	26.6	3.5	445	4	US-09-270-767-19478	Sequence 19478, A
C 687	26.8	3.5	1629	5	PCT-US91-02560-3	Sequence 3, Appli	760	26.6	3.5	486	3	US-09-522-217-3	Sequence 3, Appli
C 688	26.8	3.5	1629	3	US-09-023-655-417	Sequence 417, App	761	26.6	3.5	486	3	US-09-923-246-3	Sequence 3, Appli
C 689	26.8	3.5	1669	3	US-09-461-697-184	Sequence 184, App	762	26.6	3.5	486	3	US-10-295-723-3	Sequence 3, Appli
C 690	26.8	3.5	1716	4	US-09-248-796A-6272	Sequence 6272, Ap	763	26.6	3.5	503	4	US-09-621-976-15705	Sequence 15705, A
C 691	26.8	3.5	2099	1	US-08-299-849B-25	Sequence 25, Appl	C 764	26.6	3.5	505	4	US-09-621-976-15639	Sequence 15639, A
C 692	26.8	3.5	2099	2	US-08-142-368A-25	Sequence 25, Appl	C 765	26.6	3.5	510	4	US-09-248-796A-10295	Sequence 10295, A
C 693	26.8	3.5	2099	3	US-08-967-727-25	Sequence 25, Appl	C 766	26.6	3.5	534	3	US-09-081-180-20	Sequence 20, Appl
C 694	26.8	3.5	2099	3	US-08-037-230D-25	Sequence 25, Appl	C 767	26.6	3.5	534	3	US-09-040-786-20	Sequence 20, Appl
C 695	26.8	3.5	2099	4	US-09-583-850-25	Sequence 25, Appl	C 768	26.6	3.5	574	4	US-09-621-976-16597	Sequence 16597, A
C 696	26.8	3.5	2099	4	US-09-579-197-25	Sequence 25, Appl	C 769	26.6	3.5	599	4	US-09-270-767-3552	Sequence 3552, Ap
C 697	26.8	3.5	2099	4	US-09-404-026-25	Sequence 25, Appl	C 770	26.6	3.5	599	4	US-09-270-767-18834	Sequence 18834, A
C 698	26.8	3.5	2099	4	US-08-312-464-25	Sequence 25, Appl	C 771	26.6	3.5	669	4	US-09-328-352-2562	Sequence 2562, Ap
C 699	26.8	3.5	2150	1	US-08-299-849B-24	Sequence 24, Appl	C 772	26.6	3.5	792	4	US-09-248-796A-5468	Sequence 5468, Ap
C 700	26.8	3.5	2150	2	US-08-142-368A-24	Sequence 24, Appl	C 773	26.6	3.5	993	3	US-09-134-001C-11654	Sequence 11654, A
C 701	26.8	3.5	2150	3	US-08-967-727-24	Sequence 24, Appl	C 774	26.6	3.5	1080	4	US-08-956-171E-675	Sequence 675, App
C 702	26.8	3.5	2150	3	US-08-037-230D-24	Sequence 24, Appl	C 775	26.6	3.5	1100	4	US-08-781-986A-675	Sequence 675, App
C 703	26.8	3.5	2150	4	US-09-583-850-24	Sequence 24, Appl	C 776	26.6	3.5	1118	4	US-09-614-912-181	Sequence 181, App
C 704	26.8	3.5	2150	4	US-09-579-197-24	Sequence 24, Appl	C 777	26.6	3.5	1125	4	US-09-540-236-310	Sequence 310, App
C 705	26.8	3.5	2150	4	US-09-404-026-24	Sequence 24, Appl	C 778	26.6	3.5	1140	4	US-09-248-796A-8202	Sequence 8202, Ap
C 706	26.8	3.5	2150	4	US-09-312-464-24	Sequence 24, Appl	C 779	26.6	3.5	1149	4	US-09-716-129-38	Sequence 38, Appl
C 707	26.8	3.5	2160	1	US-08-700-749A-8	Sequence 8, Appli	C 780	26.6	3.5	1242	1	US-08-252-966B-13	Sequence 13, Appl
C 708	26.8	3.5	2160	3	US-09-020-684-8	Sequence 8, Appli	C 781	26.6	3.5	1242	4	US-09-149-476-266	Sequence 266, App
C 709	26.8	3.5	2160	3	US-09-020-467-8	Sequence 8, Appli	C 782	26.6	3.5	1262	4	US-09-134-001C-664	Sequence 664, App
C 710	26.8	3.5	2160	3	US-09-020-685-8	Sequence 8, Appli	C 783	26.6	3.5	1365	3	US-09-510-543-19	Sequence 19, Appl
C 711	26.8	3.5	2160	3	US-09-020-683-8	Sequence 8, Appli	C 784	26.6	3.5	1581	4	US-09-510-543-19	Sequence 19, Appl
C 712	26.8	3.5	2192	4	US-09-855-323-6	Sequence 6, Appli	C 785	26.6	3.5	1590	4	US-09-510-543-19	Sequence 19, Appl
C 713	26.8	3.5	2294	4	US-09-270-767-10469	Sequence 10469, A	C 786	26.6	3.5	1590	4	US-09-510-543-19	Sequence 19, Appl
C 714	26.8	3.5	2258	1	US-08-272-255-5	Sequence 5, Appli	C 787	26.6	3.5	1590	4	US-09-510-543-19	Sequence 19, Appl
C 715	26.8	3.5	2458	5	PCT-US95-08565-5	Sequence 5, Appli	C 788	26.6	3.5	1927	5	PCT-US95-13795-1	Sequence 1, Appli
C 716	26.8	3.5	2730	4	US-09-566-921-28	Sequence 28, Appl	C 789	26.6	3.5	1927	5	US-08-459-202-35	Sequence 25, Appl
C 717	26.8	3.5	2830	4	US-09-221-017B-730	Sequence 730, App	C 790	26.6	3.5	2000	1	US-08-459-202-35	Sequence 25, Appl
C 718	26.8	3.5	2894	4	US-09-138-277C-4	Sequence 4, Appli	C 791	26.6	3.5	2000	2	US-08-459-202-35	Sequence 25, Appl
C 719	26.8	3.5	2968	4	US-09-527-058-6	Sequence 6, Appli	C 792	26.6	3.5	2000	4	US-09-384-361-32	Sequence 32, Appl
C 720	26.8	3.5	3117	4	US-09-710-279-3354	Sequence 3354, Ap	C 793	26.6	3.5	2040	4	US-09-134-000C-1762	Sequence 1762, Ap
C 721	26.8	3.5	3238	3	US-08-123-934A-5	Sequence 5, Appli	C 794	26.6	3.5	2077	4	US-09-510-543-19	Sequence 19, Appl
C 722	26.8	3.5	3238	4	US-09-874-628-5	Sequence 5, Appli	C 795	26.6	3.5	2135	3	US-08-965-903B-7	Sequence 7, Appli
C 723	26.8	3.5	3238	5	PCT-US94-10080-5	Sequence 5, Appli	C 796	26.6	3.5	2149	3	US-10-101-464A-841	Sequence 841, App
C 724	26.8	3.5	3296	4	US-09-674-826B-3	Sequence 3, Appli	C 797	26.6	3.5	2340	4	US-09-620-312D-176	Sequence 176, App
C 725	26.8	3.5	3318	4	US-09-134-000C-2731	Sequence 2731, Ap	C 798	26.6	3.5	2560	4	US-09-023-655-1285	Sequence 1285, Ap
C 726	26.8	3.5	3393	3	US-09-167-109-5	Sequence 5, Appli	C 799	26.6	3.5	2570	3	US-08-974-180-14	Sequence 14, Appl
C 727	26.8	3.5	4043	4	US-09-710-279-3354	Sequence 3354, Ap	C 800	26.6	3.5	3019	4	US-09-710-279-4232	Sequence 4232, Ap
C 728	26.8	3.5	5583	4	US-09-312-283C-372	Sequence 372, App	C 801	26.6	3.5	3176	1	US-08-425-299A-3	Sequence 3, Appli
C 729	26.8	3.5	6328	3	US-08-913-832A-1	Sequence 1, Appli	C 802	26.6	3.5	3176	2	US-08-486-663A-14	Sequence 14, Appl
C 730	26.8	3.5	6328	3	US-09-249-181A-1	Sequence 1, Appli	C 803	26.6	3.5	3176	2	US-08-247-904B-13	Sequence 13, Appl
C 731	26.8	3.5	6328	4	US-09-158-707-1	Sequence 1, Appli	C 804	26.6	3.5	3176	3	US-08-767-942A-14	Sequence 14, Appl
C 732	26.8	3.5	6475	4	US-09-620-312D-325	Sequence 325, App	C 805	26.6	3.5	3348	4	US-09-710-279-3541	Sequence 3541, Ap
C 733	26.8	3.5	6766	4	US-09-527-058-1	Sequence 1, Appli	C 806	26.6	3.5	3437	1	US-08-530-950-5	Sequence 5, Appli
C 734	26.8	3.5	7432	1	US-07-852-260-1	Sequence 1, Appli	C 807	26.6	3.5	3437	4	US-09-149-879-5	Sequence 5, Appli
C 735	26.8	3.5	7432	2	US-08-461-503-1	Sequence 1, Appli	C 808	26.6	3.5	3497	4	US-09-057-009-5	Sequence 5, Appli
C 736	26.8	3.5	7432	3	US-08-465-250-1	Sequence 1, Appli	C 809	26.6	3.5	3498	3	US-08-888-429A-5	Sequence 5, Appli
C 737	26.8	3.5	7664	4	US-10-204-708-84	Sequence 84, Appl	C 810	26.6	3.5	3498	4	US-09-593-653-7	Sequence 5, Appli
C 738	26.8	3.5	8078	3	US-08-870-126-12	Sequence 12, Appl	C 811	26.6	3.5	3516	4	US-09-489-039A-3127	Sequence 3127, Ap
C 739	26.8	3.5	8078	4	US-09-445-247-12	Sequence 12, Appl	C 812	26.6	3.5	3542	1	US-09-710-279-4459	Sequence 4459, Ap
C 740	26.8	3.5	8779	4	US-08-956-171E-58	Sequence 58, Appl	C 813	26.6	3.5	3553	1	US-08-530-950-7	Sequence 7, Appli
C 741	26.8	3.5	8779	4	US-08-781-986A-58	Sequence 58, Appl	C 814	26.6	3.5	3553	3	US-09-149-879-7	Sequence 7, Appli
C 742	26.8	3.5	9706	4	US-08-843-250-5	Sequence 5, Appli	C 815	26.6	3.5	3553	4	US-09-057-009-7	Sequence 7, Appli
C 743	26.8	3.5	9841	4	US-09-843-250-3	Sequence 3, Appli	C 816	26.6	3.5	3554	3	US-08-888-429A-7	Sequence 7, Appli
C 744	26.8	3.5	12808	4	US-09-843-250-10	Sequence 10, Appl	C 817	26.6	3.5	3554	4	US-09-593-653-7	Sequence 7, Appli
C 745	26.8	3.5	14462	4	US-08-652-972A-6	Sequence 6, Appli	C 818	26.6	3.5	3576	1	US-08-530-950-9	Sequence 9, Appli
C 746	26.8	3.5	14985	1	US-08-652-972A-6	Sequence 6, Appli	C 819	26.6	3.5	3576	3	US-09-358-382-1	Sequence 1, Appli
C 747	26.8	3.5	14985	5	PCT-US96-06231A-6	Sequence 6, Appli	C 820	26.6	3.5	3576	3	US-08-888-429A-9	Sequence 9, Appli
C 748	26.8	3.5	29604	3	US-08-781-891-207	Sequence 207, App	C 821	26.6	3.5	3576	3	US-09-149-879-9	Sequence 9, Appli
C 749	26.8	3.5	29604	4	US-09-618-166-207	Sequence 207, App	C 822	26.6	3.5	3576	4	US-09-016-434-1445	Sequence 1445, Ap
C 750	26.6	3.5	189	4	US-09-248-796A-11074	Sequence 11074, A	C 823	26.6	3.5	3576	4	US-09-057-009-9	Sequence 9, Appli
C 751	26.6	3.5	228	3	US-09-134-001C-2670	Sequence 2670, Ap	C 824	26.6	3.5	3576	4	US-08-593-653-9	Sequence 9, Appli
C 752	26.6	3.5	303	4	US-08-956-171E-3033	Sequence 3033, Ap	C 825	26.6	3.5	3576	2	US-08-874-186-91	Sequence 91, Appli
C 753	26.6	3.5	303	4	US-08-781-986A-3033	Sequence 3033, Ap	C 826	26.6	3.5	3600	2	US-08-855-910-7	Sequence 7, Appli
C 754	26.6	3.5	306	4	US-09-248-796A-5114	Sequence 5114, Ap	C 827	26.6	3.5	3848	2	US-08-808-931-14	Sequence 14, Appli
C 755	26.6	3.5	354	4	US-09-489-039A-2664	Sequence 2664, Ap	C 828	26.6	3.5	3848	3	US-08-808-323-14	Sequence 14, Appli
C 756	26.6	3.5	411	4	US-09-134-000C-1810	Sequence 1810, Ap	C 829	26.6	3.5	3848	3	US-09-050-603A-14	Sequence 14, Appli
C 757	26.6	3.5	439	4	US-09-397-787-164	Sequence 164, App	C 830	26.6	3.5	3848	3	US-09-102-420B-14	Sequence 14, Appli

c 831	26.6	3.5	3848	3	US-09-497-598-14	Sequence 14, Appl	904	26.4	3.4	1269	3	US-09-134-001C-1211	Sequence 1211, Ap
c 832	26.6	3.5	3876	4	US-09-710-279-3895	Sequence 3895, Ap	905	26.4	3.4	1361	4	US-10-017-372B-36	Sequence 36, Appl
c 833	26.6	3.5	3986	4	US-09-710-279-4014	Sequence 4014, Ap	906	26.4	3.4	1361	4	US-10-017-372B-38	Sequence 38, Appl
c 834	26.6	3.5	4079	4	US-10-164-595-27	Sequence 27, Appl	c 907	26.4	3.4	1425	3	US-09-710-279-945	Sequence 945, Ap
c 835	26.6	3.5	4198	3	US-09-586-719-11	Sequence 11, Appl	c 908	26.4	3.4	1458	3	US-09-134-001C-1457	Sequence 1457, Ap
c 836	26.6	3.5	4741	1	US-07-695-472B-4	Sequence 4, Appl	c 909	26.4	3.4	1515	4	US-09-799-451-492	Sequence 492, App
c 837	26.6	3.5	4741	1	US-08-106-375-4	Sequence 4, Appl	c 910	26.4	3.4	1520	4	US-09-865-879-11	Sequence 11, Appl
c 838	26.6	3.5	4742	1	US-08-250-740-35	Sequence 35, Appl	c 911	26.4	3.4	1557	4	US-09-248-796A-5190	Sequence 5190, Ap
c 839	26.6	3.5	5111	3	US-09-004-838-118	Sequence 118, App	c 912	26.4	3.4	1565	4	US-09-149-476-134	Sequence 134, App
c 840	26.6	3.5	5224	2	US-08-874-186-46	Sequence 46, Appl	c 913	26.4	3.4	1605	4	US-09-270-767-10407	Sequence 10407, A
c 841	26.6	3.5	5857	4	US-09-220-132-79	Sequence 79, Appl	c 914	26.4	3.4	1901	3	US-09-338-907-181	Sequence 181, App
c 842	26.6	3.5	6158	4	US-09-799-451-897	Sequence 897, App	c 915	26.4	3.4	1901	3	US-09-218-207-181	Sequence 181, App
c 843	26.6	3.5	6470	4	US-09-620-312D-255	Sequence 255, App	c 916	26.4	3.4	2052	4	US-09-543-681A-1231	Sequence 1231, Ap
c 844	26.6	3.5	7646	4	US-08-956-171B-121	Sequence 121, App	c 917	26.4	3.4	2075	4	US-09-919-497-41	Sequence 41, Appl
c 845	26.6	3.5	7646	4	US-08-781-986A-121	Sequence 121, App	c 918	26.4	3.4	2141	4	US-09-841-786-11	Sequence 11, Appl
c 846	26.6	3.5	9310	4	US-08-956-171B-316	Sequence 316, App	c 919	26.4	3.4	2252	4	US-09-270-767-14448	Sequence 14448, A
c 847	26.6	3.5	9310	4	US-08-781-986A-316	Sequence 316, App	c 920	26.4	3.4	2263	4	US-09-825-497A-42	Sequence 42, Appl
c 848	26.6	3.5	9347	4	US-10-204-708-35	Sequence 35, Appl	c 921	26.4	3.4	2315	3	US-09-061-769A-1	Sequence 1, Appl
c 849	26.6	3.5	10711	4	US-08-961-527-145	Sequence 145, App	c 922	26.4	3.4	2322	3	US-09-061-769A-4	Sequence 4, Appl
c 850	26.6	3.5	15363	4	US-08-961-527-139	Sequence 139, App	c 923	26.4	3.4	2327	3	US-09-061-769A-3	Sequence 3, Appl
c 851	26.6	3.5	34794	4	US-09-713-678-39	Sequence 39, Appl	c 924	26.4	3.4	2876	3	US-08-840-204-1	Sequence 1, Appl
c 852	26.6	3.5	34794	4	US-10-002-720-44	Sequence 44, Appl	c 925	26.4	3.4	2876	3	US-08-840-204-10	Sequence 10, Appl
c 853	26.6	3.5	35828	3	US-09-449-218D-17	Sequence 17, Appl	c 926	26.4	3.4	2876	4	US-09-324-494A-1	Sequence 1, Appl
c 854	26.6	3.5	35828	4	US-09-668-529A-17	Sequence 17, Appl	c 927	26.4	3.4	2876	4	US-09-324-494A-10	Sequence 10, Appl
c 855	26.6	3.5	35828	4	US-09-668-037A-17	Sequence 17, Appl	c 928	26.4	3.4	2876	4	US-09-023-655-1187	Sequence 1187, Ap
c 856	26.6	3.5	90050	3	US-09-245-041-5	Sequence 5, Appl	c 929	26.4	3.4	2994	3	US-09-171-337A-3	GENERAL INFORMA
c 857	26.6	3.5	90050	4	US-09-358-055B-5	Sequence 5, Appl	c 930	26.4	3.4	2994	4	US-09-631-022-3	GENERAL INFORMA
c 858	26.6	3.5	90050	4	US-09-893-238-5	Sequence 5, Appl	c 931	26.4	3.4	3050	4	US-09-710-279-3815	Sequence 3815, Ap
c 859	26.4	3.4	261	4	US-09-513-999C-10755	Sequence 10755, A	c 932	26.4	3.4	3263	4	US-09-710-279-4171	Sequence 4171, Ap
c 860	26.4	3.4	309	4	US-09-313-294A-5781	Sequence 5781, Ap	c 933	26.4	3.4	3388	4	US-09-023-655-336	Sequence 336, App
c 861	26.4	3.4	335	4	US-09-513-999C-14472	Sequence 14472, A	c 934	26.4	3.4	3521	4	US-09-585-173B-35	Sequence 35, Appl
c 862	26.4	3.4	336	3	US-09-134-001C-2471	Sequence 2471, A	c 935	26.4	3.4	4042	1	US-08-200-232-1	Sequence 1, Appl
c 863	26.4	3.4	341	4	US-09-513-999C-14471	Sequence 14471, A	c 936	26.4	3.4	4042	5	PCT-US95-02219A-1	Sequence 1, Appl
c 864	26.4	3.4	350	4	US-09-203-768A-3	Sequence 3, Appl	c 937	26.4	3.4	4042	5	PCT-US95-02219A-1	Sequence 1, Appl
c 865	26.4	3.4	356	3	US-08-746-160-6	Sequence 6, Appl	c 938	26.4	3.4	4233	4	US-09-602-628-9	Sequence 9, Appl
c 866	26.4	3.4	356	3	US-08-810-324-4	Sequence 4, Appl	c 939	26.4	3.4	4972	3	US-09-035-648-17	Sequence 17, Appl
c 867	26.4	3.4	376	4	US-09-513-999C-946	Sequence 946, App	c 940	26.4	3.4	4972	3	US-09-001-951-17	Sequence 17, Appl
c 868	26.4	3.4	381	3	US-09-134-001C-1762	Sequence 1762, Ap	c 941	26.4	3.4	4972	4	US-08-818-829-17	Sequence 17, Appl
c 869	26.4	3.4	388	3	US-08-746-160-4	Sequence 4, Appl	c 942	26.4	3.4	5053	4	US-08-961-527-187	Sequence 187, App
c 870	26.4	3.4	388	3	US-08-810-324-3	Sequence 3, Appl	c 943	26.4	3.4	5219	4	US-10-204-708-51	Sequence 51, Appl
c 871	26.4	3.4	389	2	US-08-808-277A-4	Sequence 4, Appl	c 944	26.4	3.4	6669	4	US-10-204-708-6	Sequence 6, Appl
c 872	26.4	3.4	389	2	US-08-808-277A-6	Sequence 6, Appl	c 945	26.4	3.4	8334	4	US-09-543-681A-1952	Sequence 1952, Ap
c 873	26.4	3.4	390	4	US-09-311-784A-38	Sequence 38, Appl	c 946	26.4	3.4	8334	4	US-09-841-786-8	Sequence 8, Appl
c 874	26.4	3.4	396	4	US-09-248-796A-1222	Sequence 1222, Ap	c 947	26.4	3.4	11130	4	US-09-841-786-15	Sequence 15, Appl
c 875	26.4	3.4	402	1	US-08-405-034-3	Sequence 3, Appl	c 948	26.4	3.4	13205	4	US-09-835-811-3	Sequence 3, Appl
c 876	26.4	3.4	415	4	US-09-513-999C-16647	Sequence 16647, A	c 949	26.4	3.4	16550	4	US-08-916-421B-3	Sequence 3, Appl
c 877	26.4	3.4	420	4	US-09-671-317-114	Sequence 114, App	c 950	26.4	3.4	16550	4	US-09-692-570-3	Sequence 3, Appl
c 878	26.4	3.4	422	4	US-09-270-767-13938	Sequence 13938, A	c 951	26.4	3.4	31053	4	US-09-596-002-20	Sequence 20, Appl
c 879	26.4	3.4	450	3	US-08-862-124-4	Sequence 4, Appl	c 952	26.4	3.4	51719	4	US-09-518-686-2	Sequence 2, Appl
c 880	26.4	3.4	450	3	US-08-862-124-6	Sequence 6, Appl	c 953	26.4	3.4	53576	3	US-08-658-136-2	Sequence 2, Appl
c 881	26.4	3.4	501	4	US-09-107-532A-1294	Sequence 1294, Ap	c 954	26.4	3.4	53577	3	US-08-658-136-1	Sequence 1, Appl
c 882	26.4	3.4	535	4	US-08-956-171B-1028	Sequence 1028, Ap	c 955	26.4	3.4	54550	4	US-10-327-189-42	Sequence 42, Appl
c 883	26.4	3.4	535	4	US-08-781-986A-1028	Sequence 1028, Ap	c 956	26.4	3.4	56516	2	US-08-996-306-1	Sequence 1, Appl
c 884	26.4	3.4	543	4	US-09-134-000C-344	Sequence 344, App	c 957	26.4	3.4	56516	3	US-09-338-907-1	Sequence 1, Appl
c 885	26.4	3.4	555	4	US-09-270-767-998	Sequence 998, App	c 958	26.4	3.4	56516	3	US-09-218-207-1	Sequence 1, Appl
c 886	26.4	3.4	555	4	US-09-270-767-16280	Sequence 16280, A	c 959	26.4	3.4	56520	3	US-09-338-907-179	Sequence 179, App
c 887	26.4	3.4	573	4	US-09-134-000C-2670	Sequence 2670, A	c 960	26.4	3.4	56520	3	US-09-218-207-179	Sequence 179, App
c 888	26.4	3.4	597	4	US-09-543-681A-1563	Sequence 1563, Ap	c 961	26.4	3.4	70000	4	US-09-851-896-3	Sequence 3, Appl
c 889	26.4	3.4	612	4	US-09-513-999C-83	Sequence 83, Appl	c 962	26.4	3.4	81001	4	US-09-750-580-1	Sequence 1, Appl
c 890	26.4	3.4	632	4	US-09-620-312D-486	Sequence 486, App	c 963	26.4	3.4	92139	4	US-09-518-686-1	Sequence 1, Appl
c 891	26.4	3.4	708	4	US-09-472-087-40	Sequence 40, Appl	c 964	26.4	3.4	99916	4	US-09-816-095-3	Sequence 3, Appl
c 892	26.4	3.4	708	4	US-09-472-087-56	Sequence 56, Appl	c 965	26.4	3.4	152331	3	US-09-128-155-16	Sequence 16, Appl
c 893	26.4	3.4	777	4	US-09-543-681A-441	Sequence 441, App	c 966	26.4	3.4	176373	3	US-09-128-155-17	Sequence 17, Appl
c 894	26.4	3.4	819	4	US-09-107-532A-3284	Sequence 3284, Ap	c 967	26.2	3.4	179	4	US-09-621-976-15323	Sequence 15323, A
c 895	26.4	3.4	861	4	US-09-134-000C-267	Sequence 267, App	c 968	26.2	3.4	221	4	US-09-513-999C-14455	Sequence 14455, A
c 896	26.4	3.4	876	4	US-09-583-110-1540	Sequence 1540, Ap	c 969	26.2	3.4	273	4	US-09-513-999C-25314	Sequence 25314, A
c 897	26.4	3.4	909	4	US-09-107-532A-3270	Sequence 3270, Ap	c 970	26.2	3.4	308	1	US-08-225-473-4	Sequence 4, Appl
c 898	26.4	3.4	930	4	US-09-540-236-1102	Sequence 1102, Ap	c 971	26.2	3.4	339	4	US-09-513-999C-3507	Sequence 3507, Ap
c 899	26.4	3.4	1056	4	US-09-248-796A-9572	Sequence 9572, Ap	c 972	26.2	3.4	375	4	US-09-270-767-9438	Sequence 9438, Ap
c 900	26.4	3.4	1122	4	US-09-328-352-640	Sequence 640, App	c 973	26.2	3.4	375	4	US-09-270-767-24720	Sequence 24720, A
c 901	26.4	3.4	1167	4	US-09-134-000C-2473	Sequence 2473, Ap	c 974	26.2	3.4	398	4	US-09-513-999C-13068	Sequence 13068, A
c 902	26.4	3.4	1219	4	US-09-270-767-30616	Sequence 30616, A	c 975	26.2	3.4	432	4	US-09-513-999C-20111	Sequence 20111, A
c 903	26.4	3.4	1233	4	US-09-856-486-13	Sequence 13, Appl	c 976	26.2	3.4	504	4	US-09-270-767-6141	Sequence 6141, Ap

c 977	26.2	3.4	504	4	US-09-270-767-21423	Sequence 21423, A	1050	26.2	3.4	14255	1	US-08-327-392-1	Sequence 1, Appli
c 978	26.2	3.4	511	4	US-09-513-999C-10722	Sequence 10722, A	1051	26.2	3.4	14255	1	US-08-306-691B-55	Sequence 55, Appl
c 979	26.2	3.4	528	4	US-09-328-352-3188	Sequence 3188, Ap	1052	26.2	3.4	14255	3	US-08-545-860D-1	Sequence 1, Appli
c 980	26.2	3.4	564	4	US-09-621-976-225	Sequence 225, App	1053	26.2	3.4	14255	5	PCT-US94-04496-1	Sequence 1, Appli
c 981	26.2	3.4	720	4	US-09-248-796A-13544	Sequence 13544, A	1054	26.2	3.4	31728	3	US-09-453-702B-64	Sequence 64, Appl
c 982	26.2	3.4	785	4	US-09-270-767-28382	Sequence 28382, A	1055	26.2	3.4	33140	4	US-09-596-002-23	Sequence 23, Appl
c 983	26.2	3.4	816	4	US-09-270-767-13651	Sequence 4369, Ap	1056	26.2	3.4	41684	4	US-09-536-059-1	Sequence 1, Appli
c 984	26.2	3.4	825	4	US-09-270-767-13651	Sequence 19651, A	1057	26.2	3.4	42235	3	US-09-193-637A-1	Sequence 1, Appli
c 985	26.2	3.4	825	4	US-09-248-796A-10866	Sequence 10866, A	1058	26.2	3.4	161652	4	US-09-497-855A-40	Sequence 40, Appl
c 986	26.2	3.4	903	4	US-09-248-796A-4747	Sequence 4747, Ap	1059	26.2	3.4	168174	4	US-10-071-411A-63	Sequence 63, Appl
c 987	26.2	3.4	942	4	US-09-248-796A-4596	Sequence 4596, Ap	1060	26.2	3.4	168273	4	US-10-071-411A-2	Sequence 2, Appli
c 988	26.2	3.4	1019	1	US-08-225-473-2	Sequence 2, Appli	1061	26	3.4	225	4	US-09-248-796A-8831	Sequence 8831, Ap
c 989	26.2	3.4	1082	4	US-09-072-596-299	Sequence 299, App	1062	26	3.4	251	4	US-09-313-294A-1804	Sequence 1804, Ap
c 990	26.2	3.4	1082	4	US-09-072-967-304	Sequence 304, App	1063	26	3.4	314	4	US-09-513-999C-24049	Sequence 24049, A
c 991	26.2	3.4	1143	4	US-09-248-796A-2316	Sequence 2316, Ap	1064	26	3.4	344	4	US-09-513-999C-27929	Sequence 27929, A
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c 993	26.2	3.4	1227	4	US-10-222-566-1	Sequence 1, Appli	1066	26	3.4	363	4	US-09-248-796A-13221	Sequence 13221, A
c 994	26.2	3.4	1227	4	US-10-143-024A-1	Sequence 1, Appli	1067	26	3.4	426	4	US-09-710-279-1717	Sequence 1717, Ap
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c 996	26.2	3.4	1325	4	US-08-482-934A-9	Sequence 9, Appli	1069	26	3.4	445	4	US-09-270-767-22589	Sequence 22589, A
c 997	26.2	3.4	1368	4	US-09-248-796A-11323	Sequence 11323, A	1070	26	3.4	467	4	US-09-649-747A-6	Sequence 6, Appli
c 998	26.2	3.4	1383	4	US-09-543-681A-4023	Sequence 4023, Ap	1071	26	3.4	477	4	US-08-248-796A-13407	Sequence 13407, A
c 999	26.2	3.4	1440	4	US-09-248-796A-5920	Sequence 5920, Ap	1072	26	3.4	484	4	US-09-621-976-848	Sequence 848, App
1000	26.2	3.4	1669	4	US-09-149-476-133	Sequence 133, App	1073	26	3.4	493	4	US-09-513-999C-3919	Sequence 3919, Ap
c 1001	26.2	3.4	1725	4	US-09-248-796A-1180	Sequence 1180, Ap	1074	26	3.4	504	4	US-09-248-796A-5596	Sequence 5596, Ap
c 1002	26.2	3.4	1785	4	US-09-117-415B-1	Sequence 1, Appli	1075	26	3.4	534	4	US-09-583-110-1031	Sequence 1031, Ap
c 1003	26.2	3.4	1820	2	US-08-757-046A-4	Sequence 4, Appli	1076	26	3.4	571	3	US-08-858-207A-262	Sequence 262, App
c 1004	26.2	3.4	1820	3	US-09-447-208-4	Sequence 4, Appli	1077	26	3.4	604	4	US-08-288-143-62	Sequence 62, Appl
c 1005	26.2	3.4	1820	3	US-09-135-988-4	Sequence 4, Appli	1078	26	3.4	605	4	US-09-621-976-945	Sequence 945, App
c 1006	26.2	3.4	1820	3	US-09-277-716-4	Sequence 4, Appli	1079	26	3.4	621	4	US-09-270-767-23726	Sequence 23726, A
c 1007	26.2	3.4	1820	3	US-08-597-274A-4	Sequence 4, Appli	1080	26	3.4	621	4	US-09-248-796A-13224	Sequence 13224, A
c 1008	26.2	3.4	1820	4	US-08-908-909-4	Sequence 4, Appli	1081	26	3.4	723	4	US-08-224-591-11	Sequence 11, Appl
c 1009	26.2	3.4	1820	4	US-08-609-161B-4	Sequence 4, Appli	1082	26	3.4	725	2	US-08-323-388A-20	Sequence 20, Appl
c 1010	26.2	3.4	1820	4	US-08-900-103-4	Sequence 4, Appli	1083	26	3.4	725	2	US-08-926-789-11	Sequence 11, Appl
c 1011	26.2	3.4	1820	4	US-09-746-485A-4	Sequence 4, Appli	1084	26	3.4	725	3	US-09-166-750-20	Sequence 20, Appl
c 1012	26.2	3.4	1820	4	US-10-126-139-4	Sequence 4, Appli	1085	26	3.4	725	3	US-09-166-093-20	Sequence 20, Appl
c 1013	26.2	3.4	1820	4	US-10-126-798-4	Sequence 4, Appli	1086	26	3.4	725	3	US-09-166-093-20	Sequence 20, Appl
c 1014	26.2	3.4	1820	4	US-10-126-777-4	Sequence 4, Appli	1087	26	3.4	725	3	US-09-166-094-20	Sequence 20, Appl
c 1015	26.2	3.4	1842	4	US-09-117-415B-21	Sequence 21, Appl	1088	26	3.4	725	3	US-09-166-094-20	Sequence 20, Appl
c 1016	26.2	3.4	1896	4	US-09-117-415B-17	Sequence 17, Appl	1089	26	3.4	725	5	PCT-US93-11138-11	Sequence 11, Appl
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c 1019	26.2	3.4	1974	4	US-09-620-312D-256	Sequence 256, App	1092	26	3.4	731	3	US-09-166-750-10	Sequence 10, Appl
c 1020	26.2	3.4	1974	4	US-09-248-796A-5129	Sequence 5129, Ap	1093	26	3.4	731	3	US-09-166-093-10	Sequence 10, Appl
c 1021	26.2	3.4	2277	3	US-09-347-878-53	Sequence 53, Appl	1094	26	3.4	731	3	US-09-172-019-10	Sequence 10, Appl
c 1022	26.2	3.4	2310	1	US-08-471-570-9	Sequence 9, Appli	1095	26	3.4	731	3	US-09-166-094-10	Sequence 10, Appl
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c 1024	26.2	3.4	2636	4	US-09-921-259-5	Sequence 5, Appli	1097	26	3.4	755	1	US-08-323-445A-5	Sequence 5, Appli
c 1025	26.2	3.4	2876	1	US-08-471-570-7	Sequence 7, Appli	1098	26	3.4	755	1	US-08-515-903A-5	Sequence 5, Appli
c 1026	26.2	3.4	3001	3	US-09-539-333D-214	Sequence 214, App	1099	26	3.4	755	5	PCT-US95-12840-5	Sequence 5, Appli
c 1027	26.2	3.4	3191	3	US-09-453-702B-70	Sequence 70, Appl	1100	26	3.4	758	3	US-09-069-821-1	Sequence 1, Appli
c 1028	26.2	3.4	3266	3	US-08-485-511A-3	Sequence 3, Appli	1101	26	3.4	758	4	US-09-956-086-1	Sequence 1, Appli
c 1029	26.2	3.4	3416	2	US-08-451-822A-15	Sequence 15, Appl	1102	26	3.4	758	4	US-09-956-087-1	Sequence 1, Appli
c 1030	26.2	3.4	3416	3	US-08-323-430-15	Sequence 15, Appl	1103	26	3.4	782	3	US-09-420-592A-1	Sequence 1, Appli
c 1031	26.2	3.4	4183	3	US-09-460-145-1	Sequence 15, Appl	1104	26	3.4	782	4	US-09-985-442-1	Sequence 1, Appli
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c 1033	26.2	3.4	4467	1	US-08-565-907A-1	Sequence 1, Appli	1106	26	3.4	797	1	US-08-323-445A-3	Sequence 3, Appli
c 1034	26.2	3.4	4467	2	US-08-910-551B-1	Sequence 1, Appli	1107	26	3.4	797	1	US-08-515-903A-3	Sequence 3, Appli
c 1035	26.2	3.4	4467	2	US-08-909-425A-1	Sequence 1, Appli	1108	26	3.4	797	5	PCT-US95-12840-3	Sequence 3, Appli
c 1036	26.2	3.4	4983	4	US-09-270-767-12587	Sequence 12587, A	1109	26	3.4	801	4	US-09-543-681A-1732	Sequence 1732, Ap
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c 1038	26.2	3.4	5428	4	US-09-625-972-21	Sequence 21, Appl	1111	26	3.4	803	1	US-08-515-903A-7	Sequence 7, Appli
c 1039	26.2	3.4	5793	4	US-09-869-855A-3	Sequence 3, Appli	1112	26	3.4	803	5	PCT-US95-12840-7	Sequence 7, Appli
c 1040	26.2	3.4	5943	4	US-09-869-855A-2	Sequence 2, Appli	1113	26	3.4	813	1	US-08-514-014-11	Sequence 11, Appl
c 1041	26.2	3.4	6169	2	US-08-875-154-2	Sequence 2, Appli	1114	26	3.4	813	2	US-08-833-823-11	Sequence 11, Appl
c 1042	26.2	3.4	6405	4	US-09-869-855A-1	Sequence 1, Appli	1115	26	3.4	813	3	US-09-034-810-1	Sequence 1, Appli
c 1043	26.2	3.4	7260	4	US-09-917-254-31	Sequence 31, Appl	1116	26	3.4	813	3	US-08-685-239-1	Sequence 1, Appli
c 1044	26.2	3.4	7260	4	US-09-917-497-24	Sequence 24, Appl	1117	26	3.4	818	3	US-09-420-592A-3	Sequence 3, Appli
c 1045	26.2	3.4	9641	4	US-09-625-972-22	Sequence 22, Appl	1118	26	3.4	818	4	US-09-983-580-3	Sequence 3, Appli
c 1046	26.2	3.4	10216	2	US-08-875-154-1	Sequence 1, Appli	1119	26	3.4	818	4	US-09-983-580-3	Sequence 3, Appli
c 1047	26.2	3.4	11907	3	US-08-061-376-4	Sequence 4, Appli	1120	26	3.4	819	2	US-08-479-285-25	Sequence 25, Appl
c 1048	26.2	3.4	14231	4	US-08-961-527-81	Sequence 81, Appli	1121	26	3.4	819	3	US-08-479-285-25	Sequence 25, Appl
c 1049	26.2	3.4	14255	1	US-08-320-559-1	Sequence 1, Appli	1122	26	3.4	819	4	US-09-503-653A-25	Sequence 25, Appl

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1125	26	3.4	856	3	US-08-463-903-16	Sequence 16, Appl	1198	26	3.4	2165	2	US-08-263-911-8	Sequence 8, Appli
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1129	26	3.4	865	2	US-08-822-028-3	Sequence 3, Appli	1202	26	3.4	2186	4	US-09-976-594-637	Sequence 637, App
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1134	26	3.4	877	3	US-08-463-903-14	Sequence 14, Appl	1207	26	3.4	2617	1	US-09-017-302-1	Sequence 1, Appli
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1138	26	3.4	932	1	US-08-714-481-7	Sequence 7, Appli	1211	26	3.4	2696	1	US-08-321-978-1	Sequence 1, Appli
1139	26	3.4	932	5	PCT-US95-06111-7	Sequence 7, Appli	1212	26	3.4	2696	2	US-08-710-584-1	Sequence 1, Appli
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1144	26	3.4	1068	4	US-09-248-796A-9499	Sequence 9499, Ap	1217	26	3.4	3057	4	US-09-601-198-55	Sequence 55, Appl
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1146	26	3.4	1146	4	US-09-248-796A-5378	Sequence 5378, Ap	1219	26	3.4	3294	3	US-08-923-992A-7	Sequence 7, Appli
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1148	26	3.4	1237	4	US-09-620-312D-419	Sequence 419, App	1221	26	3.4	3384	3	US-08-923-992A-5	Sequence 5, Appli
1149	26	3.4	1251	4	US-09-540-236-645	Sequence 645, App	1222	26	3.4	3405	4	US-09-614-221A-425	Sequence 425, App
1150	26	3.4	1261	4	US-08-956-171B-409	Sequence 409, App	1223	26	3.4	3580	3	US-09-081-345-1	Sequence 1, Appli
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1156	26	3.4	1330	3	US-07-935-695-5	Sequence 5, Appli	1229	26	3.4	3730	5	PCT-US95-06111-8	Sequence 8, Appli
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1160	26	3.4	1346	3	US-08-463-903-9	Sequence 9, Appli	1233	26	3.4	4200	5	PCT-US95-06111-1	Sequence 1, Appli
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1162	26	3.4	1350	4	US-09-583-110-2025	Sequence 2025, Ap	1235	26	3.4	4216	4	US-09-710-279-3544	Sequence 3544, Ap
1163	26	3.4	1352	3	US-08-463-903-11	Sequence 11, Appl	1236	26	3.4	4316	4	US-08-961-527-77	Sequence 77, Appl
1164	26	3.4	1352	3	US-07-935-695-11	Sequence 11, Appl	1237	26	3.4	5619	4	US-09-614-221A-72	Sequence 72, Appl
1165	26	3.4	1359	4	US-08-961-309-69	Sequence 69, Appl	1238	26	3.4	5648	5	PCT-US96-03940-1	Sequence 1, Appli
1166	26	3.4	1361	3	US-08-463-903-21	Sequence 21, Appl	1239	26	3.4	5749	4	US-09-262-537-48	Sequence 48, Appl
1167	26	3.4	1361	3	US-07-935-695-21	Sequence 21, Appl	1240	26	3.4	5966	4	US-08-956-171B-22	Sequence 22, Appl
1168	26	3.4	1392	4	US-09-248-796A-81	Sequence 81, Appl	1241	26	3.4	5966	4	US-08-781-986A-22	Sequence 22, Appl
1169	26	3.4	1431	4	US-09-248-796A-5089	Sequence 5089, Ap	1242	26	3.4	6289	4	US-09-526-193A-26	Sequence 26, Appl
1170	26	3.4	1460	2	US-08-392-338A-18	Sequence 18, Appl	1243	26	3.4	8411	4	US-09-221-013A-3	Sequence 3, Appli
1171	26	3.4	1460	3	US-09-166-750-18	Sequence 18, Appl	1244	26	3.4	9897	4	US-08-961-527-10	Sequence 10, Appl
1172	26	3.4	1460	3	US-09-166-093-18	Sequence 18, Appl	1245	26	3.4	10726	4	US-08-961-527-66	Sequence 66, Appl
1173	26	3.4	1460	3	US-09-172-019-18	Sequence 18, Appl	1246	26	3.4	10815	3	US-09-004-838-21	Sequence 21, Appl
1174	26	3.4	1460	3	US-09-166-094-18	Sequence 18, Appl	1247	26	3.4	12730	3	US-09-004-838-91	Sequence 91, Appl
1175	26	3.4	1460	3	US-09-443-213-18	Sequence 18, Appl	1248	26	3.4	13149	3	US-09-004-838-87	Sequence 87, Appl
1176	26	3.4	1464	4	US-09-248-796A-6275	Sequence 6275, Ap	1249	26	3.4	14066	4	US-09-601-198-56	Sequence 56, Appl
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1178	26	3.4	1494	4	US-09-649-747A-10	Sequence 10, Appl	1251	26	3.4	15297	3	US-10-003-295-3	Sequence 3, Appli
1179	26	3.4	1545	4	US-09-248-796A-4080	Sequence 4080, Ap	1252	26	3.4	18443	3	US-09-078-294-6	Sequence 6, Appli
1180	26	3.4	1653	4	US-09-543-681A-2313	Sequence 2313, Ap	1253	26	3.4	23451	3	US-09-453-702B-173	Sequence 173, App
1181	26	3.4	1700	4	US-09-774-528-242	Sequence 242, App	1254	26	3.4	29555	4	US-08-956-171B-206	Sequence 206, App
1182	26	3.4	1872	3	US-09-232-200-88	Sequence 88, Appl	1255	26	3.4	29555	4	US-08-781-986A-206	Sequence 206, App
1183	26	3.4	1872	3	US-09-232-197-88	Sequence 88, Appl	1256	26	3.4	80426	3	US-09-078-294-4	Sequence 4, Appli
1184	26	3.4	1872	3	US-09-232-201-88	Sequence 88, Appl	1257	26	3.4	80595	3	US-09-078-294-3	Sequence 3, Appli
1185	26	3.4	1872	4	US-09-232-195-88	Sequence 88, Appl	1258	26	3.4	96109	4	US-09-596-002-35	Sequence 35, Appl
1186	26	3.4	1908	3	US-08-845-258-50	Sequence 50, Appl	1259	26	3.4	148567	4	US-09-801-876B-3	Sequence 3, Appli
1187	26	3.4	1908	3	US-08-990-571-50	Sequence 50, Appl	1260	26	3.4	148567	4	US-10-254-869-3	Sequence 3, Appli
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c1280	25.8	3.4	516	4	US-10-101-464A-295	Sequence 295, App	c1353	25.8	3.4	1827	4	US-09-353-688-2	Sequence 2, Appli
c1281	25.8	3.4	546	4	US-09-621-976-1811	Sequence 1811, Ap	c1354	25.8	3.4	1827	4	US-09-248-796A-6075	Sequence 6075, Ap
c1282	25.8	3.4	546	4	US-09-248-796A-1778	Sequence 1778, Ap	c1355	25.8	3.4	1863	2	US-08-455-073A-3	Sequence 3, Appli
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c1324	25.8	3.4	1001	4	US-09-641-638-558	Sequence 558, App	c1397	25.8	3.4	4773	3	US-08-884-324-9	Sequence 9, Appli
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c1340	25.8	3.4	1398	4	US-09-614-124B-322	Sequence 322, App	c1413	25.8	3.4	15297	3	US-10-003-295-3	Sequence 3, Appli
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; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
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; APPLICATION NUMBER: US/07/935,313
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; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZ9pt-F18
; US-08-232-463-14

Query Match 5.0%; Score 38.2; DB 1; Length 7218;
Best Local Similarity 5.4%; Pred. No. 0.2;
Matches 22; Conservative 207; Mismatches 180; Indels 0; Gaps 0;

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1064 GATYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1123

QY 342 ATCCATCAGGCTCTCTTAAAGTCTCTCATGTGTAATTCCTCAAGCAACAGTAATGC 401
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1124 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1183

QY 402 CAATGTGTAATTTTCATGAAACATCAGTGACATTCATCCAGATCTCTCAACTGCA 461
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1184 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1243

QY 462 GTGGTTTTCATGACCTCTGTGCACCTCCTACTGTTTCATAAACCCACAGTAAGCA 521
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1244 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1303

QY 522 CACCATCGGAGTGGCTGGAGAGCATCTAGTTTCCACTTCGATTCCTGAAGAAACAAACA 581
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1304 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1363

QY 582 TAGGCTTATCCACTCTCAGTATTTTAGTCTATGCTGTGTAATCTCGAGAGTCCT 641
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
; US-08-232-463-14

; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZ9pt-F18
; US-08-232-463-14

Query Match 5.0%; Score 38.2; DB 1; Length 7218;
Best Local Similarity 5.4%; Pred. No. 0.2;
Matches 22; Conservative 207; Mismatches 180; Indels 0; Gaps 0;

QY 282 GTTCTTCATCATTTTCAGTGTGATCACAGTCATGTGTCTGTATTCATGCTGAT 341
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1064 GATYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1123

QY 342 ATCCATCAGGCTCTCTTAAAGTCTCTCATGTGTAATTCCTCAAGCAACAGTAATGC 401
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1124 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1183

QY 402 CAATGTGTAATTTTCATGAAACATCAGTGACATTCATCCAGATCTCTCAACTGCA 461
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1184 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1243

QY 462 GTGGTTTTCATGACCTCTGTGCACCTCCTACTGTTTCATAAACCCACAGTAAGCA 521
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1244 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1303

QY 522 CACCATCGGAGTGGCTGGAGAGCATCTAGTTTCCACTTCGATTCCTGAAGAAACAAACA 581
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DB 1304 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1363

QY 582 TAGGCTTATCCACTCTCAGTATTTTAGTCTATGCTGTGTAATCTCGAGAGTCCT 641
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
; US-08-232-463-14

; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZ9pt-F18
; US-08-232-463-14

Query Match 5.0%; Score 38.2; DB 1; Length 7218;
Best Local Similarity 5.4%; Pred. No. 0.2;
Matches 22; Conservative 207; Mismatches 180; Indels 
```

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Best Local Similarity 9.6%; Pred. No. 0.35;
Matches 16; Conservative 92; Mismatches 59; Indels 0; Gaps 0;

Qy 581 ATAGGCTTATCCCACTTCTCAGTAGTATTTTGTAGTCTATTGCTGTGTGGAAATCTGGAGGTCC 640
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 19 WKWSWSYMYWKYMYMKTYWRWRKKKAWKWKYKTWTWYRYMYMGTYKKKAMCETKT 78
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 641 TGTGTTGGCTCAGTCAGATAGTCAATCGGTTTCCTTGGCTCTCTGTGTGGAGTCTCTTAAGC 700
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 79 KKKKKKGYMMYMWYWGWRSSYNAMWTRTWTGAYYRSMMYWRVRCWKKKAYYRKTTCYSS 138
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 701 GAAGAAGTCAAAATGTGTAGTATTAATGGGAATAAAATGTAAGTATCA 747
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 139 KGWTWKKRWKKAATTTWKKTYAAATRYWMMCMWTKRWASWYWCW 185
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 6
US-09-589-733C-5/c
; Sequence 5, Application US/09589733C
; Patent No. 6677503
; GENERAL INFORMATION:
; APPLICANT: Bidney, Dennis L.
; APPLICANT: Craste, Oswald R.
; APPLICANT: Davick, Jon
; APPLICANT: Hu, Xu
; APPLICANT: Lu, Guihua
; TITLE OF INVENTION: Sunflower Anti-Pathogenic Proteins and
; TITLE OF INVENTION: Genes and their Uses
; FILE REFERENCE: 5718-90
; CURRENT APPLICATION NUMBER: US/09/589,733C
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: 60/140,646
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/162,904
; PRIOR FILING DATE: 1999-11-01
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 1809
; TYPE: DNA
; ORGANISM: Helianthus annuus
US-09-589-733C-5

Query Match 4.5%; Score 34.8; DB 4; Length 1809;
Best Local Similarity 50.6%; Pred. No. 1.1;
Matches 84; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

Qy 259 TGTGCAACAACAGAACTGGAATGTTTCTTTTCATCATTTTTTCAGTGTGATCAGATCATT 318
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 988 TGGTTCAACAACGGAAGCAGTGTGTCAAATATTCCTTGATAAAATACCGTGAACAATATT 929
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 319 GGTGCTCTGATTCGATGATATCATCATCCAGGCTCTCTTAAAGGTCTCTCTCATGTGT 378
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 928 CGTACGGTTTCTGAGTGGTGTTCCTATATATCTCGGTGTTAAGCTGAACCTGTGAGT 869
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 379 AATTCTCCAAGCAACAGTAATGCAATTTGGAATTTTCATTGAAA 424
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 868 AATCAGATCAATTCGTAACACGATTTGATATTTATGGA 823
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 7
US-09-751-389-3/c
; Sequence 3, Application US/09751389
; Patent No. 6630334
; GENERAL INFORMATION:
; APPLICANT: GUGGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001067
; CURRENT APPLICATION NUMBER: US/09/751,389
; PRIOR FILING DATE: 2001-01-02
; NUMBER OF SEQ ID NOS: 8

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 786431
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(786431)
; OTHER INFORMATION: n = A,T,C or G
US-09-751-389-3

Query Match 4.5%; Score 34.2; DB 4; Length 786431;
Best Local Similarity 52.4%; Pred. No. 44;
Matches 75; Conservative 0; Mismatches 68; Indels 0; Gaps 0;
QY 387 AAGCAACAGTAAGTCCAAATTTGAAATTTTCATTGAAACATCAGTCAGATTCATCCAGA 446
Db 441396 AAGGACAGAAATGCAAGATTTCTCTCAATGTAATATACCACTGGATATACATATA 441337
QY 447 ATCCCTCAACTGTCAGTGGTTTTTCAATGACTCTTGTGCACCTCTCTACTGGTTTTCAATAA 506
Db 441336 ATTTTACATTAATAATTTTATTAACATTCCTTTGCATCTCTTAGAAGTAGTATTAA 441277
QY 507 ACCACAGTAGTACGACACCATGG 529
Db 441276 GACAATAAGACACTTCAGAAATTG 441254

RESULT 8
US-09-248-796A-2331/c
; Sequence 2331, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 2331
; LENGTH: 1284
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-2331

Query Match 4.4%; Score 33.6; DB 4; Length 1284;
Best Local Similarity 47.6%; Pred. No. 2.2;
Matches 99; Conservative 0; Mismatches 109; Indels 0; Gaps 0;
QY 556 CACTTCGATCTCGAAGAAACAAACATAGGCTATCCACTTCTCAGTATTTTAAAGTCTA 615
Db 669 CACATATTACTCAACAAACATCAAAATATCTCTATTCTGTGGTGGTGTATTCTATT 610
QY 616 TTGCTTGTGGAAATCTCGAGTCTGTTGGCTCAGTCAGATAGTCATCGGTTTCTT 675
Db 609 TGGTTTTTAGANTCATTTACGGTTGTTTAGTTTCTTGGAAATATCATATTGGTT 550
QY 676 GGCTCTGTGTGGAGTCTCTAAGCGAAGAGTCAAAATGTGTAGTTTAAATGGGAATAAA 735
Db 549 TAAACGAGAAAAGTTGATTTAAACAAATAAGTCAACAAAGTTGTGTATTGGAAGCCC 490
QY 736 ATGTAAGTATCAGTAGTTTGAARAAA 763
Db 489 ACTCAAGTATAACAATGTAGTGATAAA 462

RESULT 9
US-09-806-708B-23/c

; Sequence 23, Application US/09806708B
; Patent No. 6784342
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
; FILE REFERENCE: 4810-58741
; CURRENT APPLICATION NUMBER: US/09/806,708B
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/147,133
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 1055
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1055)
; OTHER INFORMATION: consensus sequence of A.t. and L.a. FAE1 promoters
US-09-806-708B-23

Query Match 4.3%; Score 33.2; DB 4; Length 1055;
Best Local Similarity 21.5%; Pred. No. 2.7;
Matches 47; Conservative 65; Mismatches 107; Indels 0; Gaps 0;
QY 304 GTGATCACAGTCATGGTCTCTGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAA 363
Db 233 GTTMTNNNNKAWTTTETKTMAWCAYTWTARWYTKRYTYCYATYTTYSMTYNGKMMWYWA 174
QY 364 GGTCTCTCATGTGTAATTTCTCAAGCAACAGTAATGCCAATTCGTAATTTTCATTGAAA 423
Db 173 RAAYASTNCTWSTCRWKTARGWYAYMYTWAAGSCNNNAKRCWAWYACATNNAM 114
QY 424 AACATCAGTCATTCATCCAGAAATCCTTCAACTTCGAGTGGTTTTTCAATGACTCTTGT 483
Db 113 AMWYACAYMYTAGKAATNNKTASGKMYAMMKTITWYAYWTWCAACWMAKRRRTAAK 54
QY 484 GCACCTCTACTGTTTCAATAAACCCACCAAGTAACGAC 522
Db 53 MCWYRTGYMCANNNTGRRWANCAACMAAYCANNAWCTRM 15

RESULT 10
US-09-248-796A-6609/c
; Sequence 6609, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 6609
; LENGTH: 609
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-6609

Query Match 4.3%; Score 33; DB 4; Length 609;
Best Local Similarity 55.8%; Pred. No. 2.3;
Matches 63; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
QY 412 TTTTCATTGAAAAACATCAGTCAGATTCATCCAGAAATCCTTCAACTTCGAGTGGTTTTTC 471
Db 504 TTAGATTGCCAAGCGTGATCACTTTCAAGTACAATTCATCACTTGTCTTAATGTAAG 445

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Qy 472 AATGACTCTTGTGACACCTCTACTGGTTTCAATAAACCCACGACGACAC 524
Db 444 ACTCTTGGTTTCGTAACCAATAAAGTATGCAACACACCCACCAATGACGTTAC 392

RESULT 11
US-09-710-279-3462/c
; Sequence 3462, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3462
; LENGTH: 3103
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-09-710-279-3462

Query Match 4.3%; Score 33; DB 4; Length 3103;
Best Local Similarity 55.8%; Pred. No. 5.5; Mismatches 63; Conservative 0; Indels 50; Gaps 0;

Qy 349 CAGGCTCTCTTAAAGGTCCTCTCATGTGTAATTCTCCAAGCAACAGTAATGCCAATTGT 408
Db 570 CAAGCTCTCGAATCGAATCTATCTATGTTACTTGCTCTCAGACAATACCTTTATTAAC 511

Qy 409 GAATTTTCATTGAAAAACATCAGTGACATTCATCCAGAACTCCTTCAACTTGCA 461
Db 510 TAATTTTAATATAGCAAGTCATTATCACATTTCAAGTTATTTTAAATTTGCA 458

RESULT 12
US-09-710-279-4241/c
; Sequence 4241, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4241
; LENGTH: 3438
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-09-710-279-4241

Query Match 4.3%; Score 33; DB 4; Length 3438;
Best Local Similarity 55.8%; Pred. No. 5.8; Mismatches 63; Conservative 0; Indels 50; Gaps 0;

Qy 349 CAGGCTCTCTTAAAGGTCCTCTCATGTGTAATTCTCCAAGCAACAGTAATGCCAATTGT 408
Db 2102 CAAGCTCTCTGAAATCGAATCTATCTATGTTACTTGCTCTCAGACAATACCTTTATTAAC 2043

Qy 409 GAATTTTCATTGAAAAACATCAGTGACATTCATCCAGAACTCCTTCAACTTGCA 461

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RESULT 15
US-09-513-999C-1082/c
; Sequence 1082, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Wilne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59 US2 REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 1082
; LENGTH: 414
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 118..414
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 19
; OTHER INFORMATION: s=g or c
US-09-513-999C-1082

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	Query Match	4.2%	Score 32.2;	DB 4;	Length 414;
	Best Local Similarity	56.0%;	Pred. No. 3.3;		
	Matches	61;	Conservative 0;	Mismatches 48;	Indels 0;
					Gaps 0;
QY	439	CATCAGAAATCCTTCAACTTGCAGTGGTTTTTCATGACTCTTTGGACCTCCCTACTGGT	498		
Db	150	CATCAGGAATCTCCCAACCTGCGAGTTGGACCATACTAGCGCTGCCATTTTCTTAGCTTG	91		
QY	499	TTCATAAACCACAGTACGACACATGGCGAGTGGCTGGAGAGCAT	547		
Db	90	AGCCACGCGCGGACAGGAGCGACAGCAGGGGCGACAGCGGTAAACCAT	42		

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OM nucleic - nucleic search, using sw model

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(without alignments)

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Post-processing: Minimum Match 0%

Maximum Match 100%

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- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
27	766	100.0	766	10	US-09-997-428-257
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716	766	100.0	766	15	US-10-063-550-47
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741	748.6	97.7	2294	18	US-10-331-053-35
742	747	97.5	2308	17	US-10-755-889-507
743	475.2	62.0	1504	13	US-10-087-192-62
744	475.2	62.0	1504	18	US-10-331-053-32
745	332	43.3	3262	13	US-10-087-192-64
746	332	43.3	37262	18	US-10-331-053-34
747	264.2	34.5	351	10	US-09-803-719-950
c 748	264	34.5	585	16	US-10-240-425-578
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					Sequence 950, App
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752	148.6	19.4	378	10	US-09-803-719-1159	Sequence 1159, Ap
753	69	9.0	106	9	US-09-563-817-937	Sequence 937, App
754	60	7.8	60	10	US-09-908-975-20332	Sequence 20332, A
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c 756	39.4	5.1	404	10	US-09-918-995-4534	Sequence 4534, Ap
c 757	39.4	5.1	410	10	US-09-918-995-3150	Sequence 3150, Ap
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c 764	38.2	5.0	2579	18	US-10-425-115-24879	Sequence 24879, A
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c 768	37	4.8	108182	13	US-10-087-192-1618	Sequence 1618, Ap
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c 778	35.2	4.6	655	15	US-10-027-632-251435	Sequence 251435, A
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c 821	33.4	4.4	606398	18	US-10-719-993-6782	Sequence 6782, Ap

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c 971	31.4	4.1	1313	15	US-10-164-861-112	Sequence 112, App	1044	31.2	4.1	1503841	9	US-09-795-668-1	Sequence 1, Appli
c 972	31.4	4.1	1647	16	US-10-335-977-643	Sequence 643, App	1045	31.2	4.1	1503841	9	US-09-795-668-1	Sequence 1, Appli
c 973	31.4	4.1	1737	16	US-10-335-977-644	Sequence 644, App	1046	31.2	4.1	1503841	9	US-09-795-668-1	Sequence 1, Appli
c 974	31.4	4.1	1896	16	US-10-282-1228-35397	Sequence 35397, A	c1047	31	4.0	429	18	US-10-357-930-6576	Sequence 576, Ap
c 975	31.4	4.1	1944	16	US-09-809-391-144	Sequence 391, A	c1048	31	4.0	429	18	US-10-357-930-6576	Sequence 176, App
c 976	31.4	4.1	1944	15	US-09-809-391-144	Sequence 391, A	c1049	31	4.0	429	18	US-10-357-930-6576	Sequence 176, App
c 977	31.4	4.1	1944	15	US-10-164-861-144	Sequence 144, App	c1050	31	4.0	633	13	US-10-027-632-38614	Sequence 11073, A
c 978	31.4	4.1	2307	15	US-10-032-585-6058	Sequence 6058, Ap	c1051	31	4.0	633	13	US-10-027-632-38614	Sequence 38614, A
c 979	31.4	4.1	2929	17	US-10-437-963-8855	Sequence 8855, A	c1052	31	4.0	633	15	US-10-027-632-38614	Sequence 38614, A
c 980	31.4	4.1	4562	15	US-10-037-270-418	Sequence 418, App	c1053	31	4.0	636	18	US-10-027-632-38615	Sequence 38615, A
c 981	31.4	4.1	4562	15	US-10-117-722-418	Sequence 418, App	c1054	31	4.0	636	18	US-10-027-632-38615	Sequence 38615, A
c 982	31.4	4.1	4563	18	US-10-723-860-3149	Sequence 3149, Ap	c1055	31	4.0	644	13	US-10-027-632-70034	Sequence 70034, A
c 983	31.4	4.1	4689	10	US-09-814-353-20137	Sequence 20137, A	c1056	31	4.0	644	13	US-10-027-632-70034	Sequence 70034, A
c 984	31.4	4.1	4696	18	US-10-723-860-7160	Sequence 7160, Ap	c1057	31	4.0	644	13	US-10-027-632-293899	Sequence 293899,
c 985	31.4	4.1	5464	15	US-10-111-455-1889	Sequence 1889, Ap	c1058	31	4.0	644	15	US-10-027-632-293899	Sequence 293899,
c 986	31.4	4.1	6207	16	US-10-240-454-35	Sequence 35, Appl	c1059	31	4.0	644	15	US-10-027-632-293899	Sequence 293899,
c 987	31.4	4.1	19576	16	US-10-321-613-219	Sequence 219, App	c1060	31	4.0	644	15	US-10-027-632-293899	Sequence 293899,
c 988	31.4	4.1	80077	13	US-10-087-192-1789	Sequence 1789, Ap	c1061	31	4.0	644	15	US-10-027-632-293899	Sequence 293899,
c 989	31.4	4.1	158811	18	US-10-723-860-2720	Sequence 2720, Ap	c1062	31	4.0	729	16	US-10-027-632-293899	Sequence 293899,
c 990	31.4	4.1	168325	13	US-10-087-192-955	Sequence 955, App	c1063	31	4.0	729	16	US-10-027-632-293899	Sequence 293899,
c 991	31.4	4.1	350764	13	US-10-087-192-1854	Sequence 1854, Ap	c1064	31	4.0	950	16	US-10-425-114-6157	Sequence 843, App
c 992	31.4	4.1	319	18	US-10-357-930-49133	Sequence 49133, A	c1065	31	4.0	950	16	US-10-425-114-6157	Sequence 843, App
c 993	31.2	4.1	387	18	US-10-357-930-19331	Sequence 19331, A	c1066	31	4.0	1051	16	US-10-425-114-6157	Sequence 843, App
c 994	31.2	4.1	452	10	US-09-918-995-35252	Sequence 35252, A	c1067	31	4.0	1051	16	US-10-425-114-6157	Sequence 843, App
c 995	31.2	4.1	520	15	US-10-007-926A-421	Sequence 421, App	c1068	31	4.0	1258	13	US-10-027-632-124212	Sequence 124212,
c 996	31.2	4.1	624	13	US-10-027-632-199533	Sequence 199533, A	c1069	31	4.0	1258	13	US-10-027-632-124212	Sequence 124212,
c 997	31.2	4.1	624	15	US-10-027-632-199533	Sequence 199533, A	c1070	31	4.0	1258	15	US-10-027-632-124212	Sequence 124212,
c 998	31.2	4.1	1217	18	US-10-425-115-125122	Sequence 125122, A	c1071	31	4.0	1301	16	US-10-027-632-124212	Sequence 124212,
c 999	31.2	4.1	1240	18	US-10-425-115-125122	Sequence 125122, A	c1072	31	4.0	1301	16	US-10-027-632-124212	Sequence 124212,
c 1000	31.2	4.1	1355	15	US-10-247-813-4	Sequence 4, Appli	c1073	31	4.0	1517	16	US-10-424-599-28987	Sequence 28987, A
c 1001	31.2	4.1	1547	16	US-10-425-114-25304	Sequence 25304, A	c1074	31	4.0	1561	16	US-10-425-114-19096	Sequence 19096, A
c 1002	31.2	4.1	1679	17	US-10-437-963-1263	Sequence 1263, Ap	c1075	31	4.0	1701	13	US-10-027-632-264344	Sequence 264344,
c 1003	31.2	4.1	1752	17	US-10-437-963-1263	Sequence 1263, Ap	c1076	31	4.0	1701	13	US-10-027-632-264344	Sequence 264344,
c 1004	31.2	4.1	1818	15	US-10-247-813-29	Sequence 29, Appl	c1077	31	4.0	1701	13	US-10-027-632-264344	Sequence 264344,
c 1005	31.2	4.1	2620	14	US-10-425-115-125121	Sequence 125121, A	c1078	31	4.0	1701	13	US-10-027-632-264344	Sequence 264344,
c 1006	31.2	4.1	3262	14	US-10-175-523-147	Sequence 147, App	c1079	31	4.0	1701	15	US-10-027-632-264344	Sequence 264344,
c 1007	31.2	4.1	4800	10	US-09-764-891-8780	Sequence 8780, Ap	c1080	31	4.0	1701	15	US-10-027-632-264344	Sequence 264344,
c 1008	31.2	4.1	4845	10	US-09-764-891-8781	Sequence 8781, Ap	c1081	31	4.0	1701	15	US-10-027-632-264344	Sequence 264344,
c 1009	31.2	4.1	6450	13	US-10-096-710-2	Sequence 2, Appli	c1082	31	4.0	1701	15	US-10-027-632-264344	Sequence 264344,
c 1010	31.2	4.1	6450	13	US-10-081-563-1	Sequence 1, Appli	c1083	31	4.0	1701	15	US-10-027-632-264344	Sequence 264344,
c 1011	31.2	4.1	6450	14	US-10-052-092-1	Sequence 1, Appli	c1084	31	4.0	1701	15	US-10-027-632-264344	Sequence 264344,
c 1012	31.2	4.1	6450	14	US-10-052-092-7	Sequence 7, Appli	c1085	31	4.0	1701	15	US-10-027-632-264344	Sequence 264344,
c 1013	31.2	4.1	6450	15	US-10-207-655-60	Sequence 60, Appl	c1086	31	4.0	2561	16	US-10-424-599-104907	Sequence 104907,
c 1014	31.2	4.1	6450	15	US-10-177-293-127	Sequence 127, App	c1087	31	4.0	3051	17	US-10-424-599-66239	Sequence 66239, A
c 1015	31.2	4.1	6450	15	US-10-027-983-3	Sequence 3, Appli	c1088	31	4.0	3316	15	US-10-424-599-66239	Sequence 66239, A
c 1016	31.2	4.1	6450	15	US-10-007-926A-422	Sequence 422, App	c1089	31	4.0	4386	17	US-10-424-599-66239	Sequence 66239, A
c 1017	31.2	4.1	6450	15	US-10-437-107-1	Sequence 1, Appli	c1090	31	4.0	4386	17	US-10-424-599-66239	Sequence 66239, A
c 1018	31.2	4.1	6450	15	US-10-437-107-7	Sequence 7, Appli	c1091	31	4.0	4386	17	US-10-424-599-66239	Sequence 66239, A
c 1019	31.2	4.1	6450	15	US-10-392-274-1	Sequence 1, Appli	c1092	31	4.0	4386	17	US-10-424-599-66239	Sequence 66239, A
c 1020	31.2	4.1	6450	15	US-10-448-753-3	Sequence 3, Appli	c1093	31	4.0	4386	17	US-10-424-599-66239	Sequence 66239, A
c 1021	31.2	4.1	6450	15	US-10-472-118-435	Sequence 435, App	c1094	31	4.0	4386	17	US-10-424-599-66239	Sequence 66239, A
c 1022	31.2	4.1	6450	15	US-10-488-360-303	Sequence 303, App	c1095	31	4.0	4386	17	US-10-424-599-66239	Sequence 66239, A
c 1023	31.2	4.1	6450	16	US-10-342-887-435	Sequence 435, App	c1096	31	4.0	4386	17	US-10-424-599-66239	Sequence 66239, A
c 1024	31.2	4.1	6450	18	US-10-370-715B-75	Sequence 75, Appl	c1097	31	4.0	4386	17	US-10-424-599-66239	Sequence 66239, A
c 1025	31.2	4.1	6450	18	US-10-896-419-1	Sequence 1, Appli	c1098	31	4.0	4386	17	US-10-424-599-66239	Sequence 66239, A
c 1026	31.2	4.1	6450	18	US-10-896-419-7	Sequence 7, Appli	c1099	31	4.0	4386	17	US-10-424-599-66239	Sequence 66239, A
c 1027	31.2	4.1	6608	14	US-10-198-846-11305	Sequence 11305, A	c1100	31	4.0	4386	17	US-10-424-599-66239	Sequence 66239, A
c 1028	31.2	4.1	8566	15	US-10-027-983-10	Sequence 10, Appl	c1101	31	4.0	4386	17	US-10-424-599-66239	Sequence 66239, A
c 1029	31.2	4.1	8566	15	US-10-448-753-10	Sequence 10, Appl	c1102	31	4.0	4386	17	US-10-424-599-66239	Sequence 66239, A
c 1030	31.2	4.1	22073	10	US-09-764-891-7351	Sequence 7351, Ap	c1103	31	4.0	4386	17	US-10-424-599-66239	Sequence 66239, A
c 1031	31.2	4.1	30304	17	US-10-367-094-128	Sequence 128, App	c1104	31	4.0	4386	17	US-10-424-599-66239	Sequence 66239, A
c 1032	31.2	4.1	54810	18	US-10-417-375-91	Sequence 91, Appl	c1105	31	4.0	4386	17	US-10-424-599-66239	Sequence 66239, A
c 1033	31.2	4.1	108664	14	US-10-175-523-97	Sequence 97, Appl	c1106	31	4.0	4386	17	US-10-424-599-66239	Sequence 66239, A
c 1034	31.2	4.1	247682	9	US-09-731-231A-3	Sequence 28, Appl	c1107	31	4.0	4386	17	US-10-424-599-66239	Sequence 66239, A
c 1035	31.2	4.1	326014	16	US-10-235-192A-28	Sequence 3, Appli	c1108	31	4.0	4386	17	US-10-424-599-66239	Sequence 66239, A
c 1036	31.2	4.1	326014	17	US-10-751-985-3	Sequence 3, Appli	c1109	31	4.0	4386	17	US-10-424-599-66239	Sequence 66239, A
c 1037	31.2	4.1	392000	15	US-10-027-983-11	Sequence 11, Appl	c1110	31	4.0	4386	17	US-10-424-599-66239	Sequence 66239, A
c 1038	31.2	4.1	392000	15	US-10-448-753-11	Sequence 11, Appl	c1111	31	4.0	4386	17	US-10-424-599-66239	Sequence 66239, A
c 1039	31.2	4.1	455237	9	US-09-933-267A-1	Sequence 11, Appl	c1112	31	4.0	4386	17	US-10-424-599-66239	Sequence 66239, A
c 1040	31.2	4.1	653122	13	US-10-087-192-226	Sequence 226, App	c1113	31	4.0	4386	17	US-10-424-599-66239	Sequence 66239, A

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c1121	30.8	4.0	381	18	US-10-425-115-44413	Sequence 44413, A	1194	30.8	4.0	435	18	US-10-357-930-32875	Sequence 32875, A
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1128	30.8	4.0	385	18	US-10-357-930-32833	Sequence 32833, A	1201	30.8	4.0	440	18	US-10-357-930-41801	Sequence 41801, A
1129	30.8	4.0	388	18	US-10-357-930-10513	Sequence 10513, A	1202	30.8	4.0	440	18	US-10-357-930-42036	Sequence 42036, A
1130	30.8	4.0	390	16	US-10-424-599-91710	Sequence 91710, A	1203	30.8	4.0	440	18	US-10-357-930-42036	Sequence 42036, A
1131	30.8	4.0	390	18	US-10-357-930-2987	Sequence 2987, Ap	1204	30.8	4.0	441	18	US-10-357-930-3263	Sequence 3263, Ap
1132	30.8	4.0	391	18	US-10-357-930-2725	Sequence 2725, Ap	1205	30.8	4.0	441	18	US-10-357-930-37013	Sequence 37013, A
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1134	30.8	4.0	391	18	US-10-357-930-11890	Sequence 11890, A	1207	30.8	4.0	443	18	US-10-357-930-32718	Sequence 32718, A
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c1137	30.8	4.0	394	16	US-10-424-599-113745	Sequence 113745, A	1210	30.8	4.0	445	18	US-10-357-930-2769	Sequence 2769, Ap
1138	30.8	4.0	395	18	US-10-357-930-15391	Sequence 15391, A	1211	30.8	4.0	446	18	US-10-357-930-33189	Sequence 33189, A
1139	30.8	4.0	396	18	US-10-357-930-11812	Sequence 11812, A	1212	30.8	4.0	446	18	US-10-357-930-41865	Sequence 41865, A
1140	30.8	4.0	397	18	US-10-357-930-11938	Sequence 11938, A	1213	30.8	4.0	446	18	US-10-357-930-42114	Sequence 42114, A
1141	30.8	4.0	398	18	US-10-357-930-11546	Sequence 11546, A	1214	30.8	4.0	447	18	US-10-357-930-32988	Sequence 32988, A
1142	30.8	4.0	398	18	US-10-357-930-11592	Sequence 11592, A	1215	30.8	4.0	450	18	US-10-357-930-2647	Sequence 2647, Ap
1143	30.8	4.0	399	18	US-10-357-930-12017	Sequence 12017, A	1216	30.8	4.0	452	18	US-10-357-930-31426	Sequence 31426, Ap
1144	30.8	4.0	400	18	US-10-357-930-2805	Sequence 2805, Ap	1217	30.8	4.0	452	18	US-10-357-930-40396	Sequence 40396, A
1145	30.8	4.0	401	18	US-10-357-930-11703	Sequence 11703, A	1218	30.8	4.0	453	18	US-10-357-930-1059	Sequence 1059, Ap
1146	30.8	4.0	402	18	US-10-357-930-32697	Sequence 32697, A	c1219	30.8	4.0	459	16	US-10-424-599-51631	Sequence 51631, A
1147	30.8	4.0	402	18	US-10-357-930-2900	Sequence 2900, Ap	1220	30.8	4.0	462	18	US-10-357-930-33445	Sequence 33445, A
1148	30.8	4.0	402	18	US-10-357-930-11974	Sequence 11974, A	1221	30.8	4.0	463	18	US-10-357-930-33326	Sequence 33326, A
1149	30.8	4.0	402	18	US-10-357-930-31447	Sequence 31447, A	1222	30.8	4.0	464	18	US-10-357-930-40331	Sequence 40331, A
1150	30.8	4.0	402	18	US-10-357-930-3382	Sequence 3382, A	1223	30.8	4.0	464	18	US-10-357-930-33366	Sequence 33366, A
1151	30.8	4.0	406	18	US-10-357-930-2529	Sequence 2529, Ap	1224	30.8	4.0	464	18	US-10-357-930-40417	Sequence 40417, A
1152	30.8	4.0	406	18	US-10-357-930-11816	Sequence 11816, A	1225	30.8	4.0	464	18	US-10-357-930-40580	Sequence 40580, A
1153	30.8	4.0	407	18	US-10-357-930-2377	Sequence 2377, Ap	1226	30.8	4.0	464	18	US-10-357-930-40679	Sequence 40679, A
1154	30.8	4.0	407	18	US-10-357-930-33245	Sequence 33245, A	1227	30.8	4.0	464	18	US-10-357-930-42230	Sequence 42230, A
1155	30.8	4.0	407	18	US-10-357-930-42169	Sequence 42169, A	1228	30.8	4.0	468	18	US-10-357-930-45072	Sequence 45072, A
1156	30.8	4.0	410	18	US-10-357-930-10228	Sequence 10228, A	1229	30.8	4.0	468	18	US-10-357-930-33356	Sequence 33356, A
1157	30.8	4.0	410	18	US-10-357-930-12154	Sequence 12154, A	1230	30.8	4.0	469	18	US-10-357-930-40461	Sequence 40461, A
1158	30.8	4.0	411	18	US-10-357-930-6222	Sequence 6222, Ap	1231	30.8	4.0	469	18	US-10-357-930-42385	Sequence 42385, A
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1160	30.8	4.0	414	18	US-10-357-930-32943	Sequence 32943, A	1233	30.8	4.0	484	13	US-10-027-632-194226	Sequence 194226, A
1161	30.8	4.0	414	18	US-10-357-930-41869	Sequence 41869, A	1234	30.8	4.0	484	15	US-10-027-632-194226	Sequence 194226, A
1162	30.8	4.0	416	18	US-10-357-930-2848	Sequence 2848, Ap	1235	30.8	4.0	496	18	US-10-357-930-6642	Sequence 6642, Ap
1163	30.8	4.0	416	18	US-10-357-930-32870	Sequence 32870, A	1236	30.8	4.0	504	18	US-10-357-930-60388	Sequence 60388, A
1164	30.8	4.0	417	18	US-10-357-930-2721	Sequence 2721, Ap	1237	30.8	4.0	517	18	US-10-357-930-39191	Sequence 39191, A
c1165	30.8	4.0	418	18	US-10-674-124A-1922	Sequence 1922, Ap	1238	30.8	4.0	520	18	US-10-357-930-36617	Sequence 36617, A
1166	30.8	4.0	418	18	US-10-357-930-33328	Sequence 33328, A	1239	30.8	4.0	520	18	US-10-357-930-41623	Sequence 41623, A
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1168	30.8	4.0	419	18	US-10-357-930-994	Sequence 994, App	1241	30.8	4.0	541	18	US-10-357-930-6793	Sequence 6793, Ap
1169	30.8	4.0	419	18	US-10-357-930-31611	Sequence 31611, A	1242	30.8	4.0	560	13	US-10-027-632-41707	Sequence 41707, A
1170	30.8	4.0	419	18	US-10-357-930-32704	Sequence 32704, A	c1243	30.8	4.0	562	16	US-10-027-632-41707	Sequence 41707, A
1171	30.8	4.0	419	18	US-10-357-930-41796	Sequence 41796, A	1244	30.8	4.0	565	18	US-10-357-930-2697	Sequence 2697, Ap
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1174	30.8	4.0	421	18	US-10-357-930-32967	Sequence 32967, A	1247	30.8	4.0	578	10	US-09-814-353-1164	Sequence 1164, A
1175	30.8	4.0	422	18	US-10-357-930-12273	Sequence 12273, A	c1248	30.8	4.0	584	13	US-10-027-632-41690	Sequence 41690, A
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1177	30.8	4.0	423	18	US-10-357-930-2643	Sequence 2643, Ap	c1250	30.8	4.0	584	15	US-10-027-632-41690	Sequence 41690, A
c1178	30.8	4.0	427	9	US-09-736-457-1152	Sequence 1152, Ap	c1251	30.8	4.0	584	15	US-10-027-632-41691	Sequence 41691, A
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c1412	30.4	4.0	308	9	US-09-954-531-263	Sequence 263, Appl	1485	30.4	4.0	15387	15	US-10-311-455-158	Sequence 158, Appl
c1413	30.4	4.0	308	10	US-09-873-367C-407	Sequence 407, Appl	1486	30.4	4.0	15767	15	US-10-311-455-1180	Sequence 1180, Appl
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1421	30.4	4.0	599	15	US-10-027-632-113736	Sequence 113736,	c1494	30.2	3.9	268	16	US-10-424-599-105307	Sequence 105307,
1422	30.4	4.0	599	15	US-10-027-632-113734	Sequence 113734,	1495	30.2	3.9	270	16	US-10-242-535A-54892	Sequence 54892, A
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c1425	30.4	4.0	604	17	US-10-767-701-22180	Sequence 22180, A	1498	30.2	3.9	455	13	US-10-027-632-321068	Sequence 321068,
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Search completed: January 24, 2005, 19:16:04
Job time : 419 secs

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OM nucleic - nucleic search, using sw model

Run on: January 24, 2005, 18:16:31 ; Search time 2066 Seconds
(without alignments)
13510.569 Million cell updates/sec

Title: US-10-063-553-47

Perfect score: 766

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Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

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1: gb_est1:*

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7: gb_est6:*

8: gb_gss1:*

9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	647.4	84.5	907	7	CO582275 ILLUMIGEN
5	642.6	83.9	924	7	CO644900 ILLUMIGEN
6	634.6	82.8	1006	4	BM923940 AGENCOURT
7	610.2	79.7	896	7	CO582384 ILLUMIGEN
8	496	64.8	713	7	CN793461 4128489 B
9	493.6	64.4	888	7	CO580240 ILLUMIGEN
10	492.2	64.3	705	7	CN786443 4120438 B
11	487.2	63.6	726	7	CK837742 4062718 B
12	476.8	62.2	1505	3	AK007532 Mus muscu
13	475.2	62.0	1471	3	AK017195 Mus muscu
14	473.8	61.9	972	6	BY707590 BY707590
15	473.6	61.8	796	3	AK017154 Mus muscu
16	473.2	61.8	763	6	BY716940 BY716940
17	470.2	61.4	759	3	AK017209 Mus muscu
18	463.2	60.5	682	7	CK959274 4100113 B
19	461.8	60.3	465	5	BX483390 DXFZ686C
20	452.4	59.1	691	7	CK946479 4071113 B
21	435.8	56.9	639	7	CN788764 4123131 B
22	431	56.3	433	1	AI380663 t597c01.x
23	427.4	55.8	856	7	CK459335 923831 WA
24	414.6	54.1	738	5	BQ198769 UI-R-EB0-

CN542594	UI-R-EB0-	727	7	CN542594
BQ198759	UI-R-EB0-	747	5	BQ198759
BF577384	602092211	957	7	BF577384
BM768647	K-EST0051	402	4	BM768647
BY716926	BY716926	663	6	BY716926
AI480436	vg20b09.x	571	1	AI480436
BX512971	BX512971	542	5	BX512971
AA823516	VP41C11.r	537	1	AA823516
BM385993	UI-R-DN1-	573	4	BM385993
AW142069	EST292284	548	2	AW142069
CK946446	4070729 B	669	7	CK946446
BE135672	ug54a06.y	513	2	BE135672
AA871783	vg40h12.r	504	1	AA871783
CB223209	1JBJ20H4	493	6	CB223209
CG494845	OST33941	536	9	CG494845
AA233015	mk01909.r	472	1	AA233015
AA233015	mk36h07.r	476	1	AA233015
CK457599	921911 MA	748	7	CK457599
AI613849	vg20b09.y	471	1	AI613849
CK959073	4099729 B	639	7	CK959073
BE135674	ug54a08.y	435	2	BE135674
CN792529	4127403 B	665	7	CN792529
BM087683	500492 MA	460	4	BM087683
AI013728	EST208403	494	1	AI013728
AA801387	EST190884	432	1	AA801387
BE138229	vg39a02.r	484	1	BE138229
AA813626	ug50e02.y	457	2	AA813626
CK945394	4069645 B	634	7	CK945394
BM432584	1JBJ11D8.	376	4	BM432584
AA871986	vg47h12.r	441	1	AA871986
AI346656	qp52b03.x	585	1	AI346656
AA801386	EST190883	453	1	AA801386
BY077642	BY077642	372	5	BY077642
CK837956	4062969 B	736	7	CK837956
AA509688	vg20b09.r	353	1	AA509688
CE024812	tigr-gss-	741	9	CE024812
BE136789	ug50e02.x	380	2	BE136789
BE198833	ug54a08.x	369	2	BE198833
CR468081	CR468081	370	7	CR468081
CB697042	AMGNNUC.C	310	6	CB697042
CO259142	4130488 B	231	7	CO259142
AA709891	vt35d03.r	389	1	AA709891
CK945207	4069261 B	611	7	CK945207
BE686508	uu68h08.x	502	2	BE686508
CN792346	4127194 B	478	7	CN792346
CB983935	AGENCOURT	756	6	CB983935
BB574464	BB574464	255	2	BB574464
CG590198	OST243329	243	9	CG590198
AI346667	qp52c03.x	459	1	AI346667
CK949720	4074836 B	653	7	CK949720
CF590786	AGENCOURT	798	7	CF590786
AV288247	AV288247	235	1	AV288247
CO051441	Le.mxo.27	709	7	CO051441
CF591902	AGENCOURT	802	7	CF591902
BU026491	OHG17A0A.	407	5	BU026491
AV290031	AV290031	222	1	AV290031
BZ898723	CH240.14P	585	8	BZ898723
AW914486	EST345790	1126	2	AW914486
CG586595	OST235323	233	9	CG586595
CE157568	tigr-gss-	747	9	CE157568
BZ945484	CH240.122	470	8	BZ945484
BG713387	pgl1n.pk0	591	4	BG713387
BU243566	603778448	778	5	BU243566
BUI25951	603150146	832	5	BUI25951
BU240401	60323083	731	5	BU240401
CF662407	CcLL01a04	863	7	CF662407
CK833599	4057710 B	506	7	CK833599
BE331646	sp17c05.y	478	2	BE331646
BX821771	ArabiDops	925	3	BX821771
AL070833	Drosophila	1101	9	AL070833
CB650785	OSUNEB15G	782	6	CB650785
CB655796	OSUNEC091	863	6	CB655796
AL108333	Drosophila	1072	9	AL108333

c 98	39.4	5.1	776	7	CF596979	AGENCYCOURT	c 171	36.2	4.7	959	9	CNS003FH	AL064543	Drosophil
c 99	39.4	5.1	1128	7	CF596976	AGENCYCOURT	172	36	4.7	149	5	BX255782	BX255782	BX255782
c 100	39.2	5.1	281	2	BB516670	BB516670	c 173	36	4.7	252	2	BB036514	BB036514	BB036514
c 101	39.2	5.1	291	2	BB375714	BB375714	c 174	36	4.7	266	2	BB006979	BB006979	BB006979
c 102	39.2	5.1	578	1	AL725209	1228 PtIF	c 175	36	4.7	283	1	AV325550	AV325550	AV325550
c 103	39	5.1	453	2	AW703939	sk14a06.Y	c 176	36	4.7	332	2	BB115991	BB115991	BB115991
c 104	39	5.1	478	7	CN792346	4127194 B	c 177	36	4.7	471	4	BJ094908	BJ094908	BJ094908
c 105	39	5.1	1204	9	CNS016E2	AL106628 Drosophil	c 178	36	4.7	545	5	BY470456	BY470456	BY470456
c 106	38.8	5.1	613	4	BJ407375	BJ407375	c 179	36	4.7	690	8	BH208184	BH208184	BH208184
c 107	38.8	5.1	671	5	BX302895	BX302895	c 180	36	4.7	815	9	CG974124	CG974124	CG974124
c 108	38.8	5.1	814	4	BE784777	SEADMC004	c 181	36	4.7	826	7	CN182549	CN182549	CN182549
c 109	38.2	5.0	570	6	CF314664	ABF--08-1	c 182	36	4.7	1080	9	AL069494	AL069494	AL069494
c 110	38.2	5.0	648	2	AW497882	AW497882	c 183	36	4.7	1201	9	AL098625	AL098625	AL098625
c 111	38.2	5.0	671	5	BX866069	BX866069	c 184	35.8	4.7	750	1	AV930455	AV930455	AV930455
c 112	38.2	5.0	766	5	BX861486	BX861486	c 185	35.8	4.7	751	4	BI888233	BI888233	BI888233
c 113	38.2	5.0	789	5	BX302266	BX302266	c 186	35.8	4.7	765	8	AO935034	AO935034	AO935034
c 114	38.2	5.0	866	6	CB633487	OS11E512F	c 187	35.8	4.7	810	8	AO935014	AO935014	AO935014
c 115	38	5.0	688	7	CO080632	GR_E44D	c 188	35.8	4.7	896	8	AZ674070	AZ674070	AZ674070
c 116	38	5.0	937	9	CNS0207W	AL206357 Tetraodon	c 189	35.8	4.7	2721	3	AK090149	AK090149	AK090149
c 117	37.6	4.9	135	5	BX249501	BX249501	c 190	35.6	4.6	324	5	EX689205	EX689205	EX689205
c 118	37.6	4.9	285	2	BB074742	BB074742	c 191	35.6	4.6	470	6	CF096856	CF096856	CF096856
c 119	37.6	4.9	363	1	AA279774	z92e09.s	c 192	35.6	4.6	504	8	AZ165656	AZ165656	AZ165656
c 120	37.6	4.9	376	5	BX254242	BX254242	c 193	35.6	4.6	523	2	AW648555	AW648555	AW648555
c 121	37.6	4.9	377	5	BX249146	BX249146	c 194	35.6	4.6	543	4	BJ221482	BJ221482	BJ221482
c 122	37.6	4.9	377	5	BX250874	BX250874	c 195	35.6	4.6	638	6	CB681060	CB681060	CB681060
c 123	37.6	4.9	498	5	BX254094	BX254094	c 196	35.6	4.6	674	9	AG124666	AG124666	AG124666
c 124	37.6	4.9	798	5	BX252143	BX252143	c 197	35.6	4.6	683	4	BJ714182	BJ714182	BJ714182
c 125	37.4	4.9	232	8	B58259	CIT-HSP-201	c 198	35.6	4.6	737	5	BU144245	BU144245	BU144245
c 126	37.4	4.9	532	8	AL78439	HS_2223.A	c 199	35.6	4.6	737	5	AG165651	AG165651	AG165651
c 127	37.4	4.9	815	9	CC592084	CH240_392	c 200	35.6	4.6	807	9	BU113228	BU113228	BU113228
c 128	37.4	4.9	1009	9	CL135224	ISH1-106D	c 201	35.6	4.6	833	5	BE541205	BE541205	BE541205
c 129	37.4	4.9	1101	9	CNS00B4E	AL056409 Drosophil	c 202	35.6	4.6	952	2	AG382614	AG382614	AG382614
c 130	37.4	4.9	1571	8	CL189486	CH261-36F	c 203	35.6	4.6	1061	9	BB552635	BB552635	BB552635
c 131	37.2	4.9	446	6	CF097240	CHN3118.Y	c 204	35.4	4.6	299	2	BJ415704	BJ415704	BJ415704
c 132	37.2	4.9	525	6	CF096471	CHN23E21.	c 205	35.4	4.6	400	4	BF517773	BF517773	BF517773
c 133	37.2	4.9	589	6	CB489888	omykrifh0	c 206	35.4	4.6	507	2	AL067971	AL067971	AL067971
c 134	37.2	4.9	625	4	BJ501925	BJ501925	c 207	35.4	4.6	603	1	AI066689	AI066689	AI066689
c 135	37.2	4.9	640	6	CB489716	omykrifh0	c 208	35.4	4.6	645	1	AV400694	AV400694	AV400694
c 136	37.2	4.9	747	5	CB081390	CB081390	c 209	35.4	4.6	839	1	AZ680660	AZ680660	AZ680660
c 137	37	4.8	459	1	AL819077	AL819077	c 210	35.4	4.6	860	2	BE543834	BE543834	BE543834
c 138	37	4.8	583	6	CB484793	hab91803.	c 211	35.4	4.6	922	2	CL064547	CL064547	CL064547
c 139	37	4.8	686	1	AL962933	AL962933	c 212	35.4	4.6	967	9	CNS00EHN	CNS00EHN	CNS00EHN
c 140	37	4.8	725	9	AJ589115	AJ589115 Arabidops	c 213	35.4	4.6	1101	5	EX504843	EX504843	EX504843
c 141	37	4.8	860	8	AQ741470	HS_5571.B	c 214	35.2	4.6	267	5	CR140345	CR140345	CR140345
c 142	36.8	4.8	864	8	CC098399	CSU_K34.1	c 215	35.2	4.6	533	9	EX997368	EX997368	EX997368
c 143	36.8	4.8	1059	9	CL014259	ZMWB0054	c 216	35.2	4.6	543	9	CR006073	CR006073	CR006073
c 144	36.8	4.8	1230	1	AJ301029	AJ301029	c 217	35.2	4.6	582	8	AQ855803	AQ855803	AQ855803
c 145	36.6	4.8	363	1	AL438356	SWOVAFCAP	c 218	35.2	4.6	621	8	AZ523380	AZ523380	AZ523380
c 146	36.6	4.8	371	1	AT002520	AT002520	c 219	35.2	4.6	689	7	CF517318	CF517318	CF517318
c 147	36.6	4.8	401	5	BX501776	DFZp7790	c 220	35.2	4.6	690	9	CR034409	CR034409	CR034409
c 148	36.6	4.8	491	2	BF228854	qc64a10.b	c 221	35.2	4.6	733	9	CR140345	CR140345	CR140345
c 149	36.6	4.8	533	5	BO793354	EST_2292	c 222	35.2	4.6	778	9	EX997368	EX997368	EX997368
c 150	36.6	4.8	592	2	BE595816	P11_54.D1	c 223	35.2	4.6	780	9	CR027870	CR027870	CR027870
c 151	36.6	4.8	642	4	BM079639	MEST97-D0	c 224	35.2	4.6	781	5	EX870144	EX870144	EX870144
c 152	36.6	4.8	699	6	CA079235	SCSBAM108	c 225	35.2	4.6	844	9	EX984820	EX984820	EX984820
c 153	36.6	4.8	702	6	CA264459	SCQGLB204	c 226	35.2	4.6	861	5	BU938050	BU938050	BU938050
c 154	36.6	4.8	808	9	CR242329	Reverse.s	c 227	35.2	4.6	864	5	CNS00BZ9	CNS00BZ9	CNS00BZ9
c 155	36.6	4.8	963	3	AV105617	Zea.mays	c 228	35.2	4.6	865	9	CR179050	CR179050	CR179050
c 156	36.6	4.8	1358	9	CL022089	CH216-13K	c 229	35.2	4.6	865	9	CR179050	CR179050	CR179050
c 157	36.6	4.8	626	5	BQ340646	PMO-NN025	c 230	35	4.6	388	5	BQ601153	BQ601153	BQ601153
c 158	36.4	4.8	652	7	CO125984	GR_EB09M	c 231	35	4.6	414	4	BI401520	BI401520	BI401520
c 159	36.4	4.8	707	9	CL558902	OB_Ba001	c 232	35	4.6	449	5	EX866115	EX866115	EX866115
c 160	36.4	4.8	780	4	BI335415	602597993	c 233	35	4.6	452	5	BQ600175	BQ600175	BQ600175
c 161	36.2	4.7	409	6	CA924119	MTU7CL.P1	c 234	35	4.6	457	8	CC063063	CC063063	CC063063
c 162	36.2	4.7	452	5	BU895153	X02A05.P	c 235	35	4.6	514	1	AL923204	AL923204	AL923204
c 163	36.2	4.7	468	6	CF097930	QHN5L07.Y	c 236	35	4.6	517	5	BQ603905	BQ603905	BQ603905
c 164	36.2	4.7	493	2	BF707083	281793.MA	c 237	35	4.6	544	9	CE230261	CE230261	CE230261
c 165	36.2	4.7	567	9	CR249441	Forward.s	c 238	35	4.6	592	5	BF772239	BF772239	BF772239
c 166	36.2	4.7	586	1	AT691314	606014B10	c 239	35	4.6	595	2	BM712293	BM712293	BM712293
c 167	36.2	4.7	613	6	CA923569	MTU7CL.P1	c 240	35	4.6	612	4	BM246575	BM246575	BM246575
c 168	36.2	4.7	613	6	CA923949	MTU7CL.P1	c 241	35	4.6	619	2	AW885920	AW885920	AW885920
c 169	36.2	4.7	844	4	BF676512	602084417	c 242	35	4.6	651	2	BB037184	BB037184	BB037184
c 170	36.2	4.7	948	9	CNS0159T	AL105179 Drosophil	c 243	35	4.6	667	7	CN9039726	CN9039726	CN9039726

C 244	681	9	CR001380	Forward s	317	34.6	4.5	457	7	T88391	T88391 12087 Lambda
C 245	791	6	CD776245	UI-M-AQ0-	C 318	34.6	4.5	528	4	BI128486	BI128486 G076P74Y
C 246	791	6	BX209122	Danio rer	C 319	34.6	4.5	555	7	CK102412	CK102412 G076P74.5
C 247	795	8	BH603746	BOGEL51TR	320	34.6	4.5	571	5	BW778992	BW778992 SJEES02
C 248	830	8	CK109681	NDL.29P17	321	34.6	4.5	615	5	CA926534	CA926534 MTU6CR.P1
C 249	1509	3	CNS0A9PM	Arabidops	C 322	34.6	4.5	617	9	CE700116	CE700116 tigr-g88-
C 250	1526	3	CNS0A9KO	Arabidops	C 323	34.6	4.5	637	4	BG974431	BG974431 602844212
C 251	2142	3	AK031184	Mus muscu	324	34.6	4.5	642	4	BG973919	BG973919 602843555
C 252	217	4	AG098616	EST463135	325	34.6	4.5	658	5	BX352728	BX352728 BX252728
C 253	221	1	AV338652	AV338652	326	34.6	4.5	666	4	BI661990	BI661990 603304985
C 254	293	5	BW721081	BW721081	327	34.6	4.5	681	4	BG861503	BG861503 602795465
C 255	294	5	BQ451988	PFEStOaa9	328	34.6	4.5	681	4	BG915006	BG915006 602813879
C 256	333	5	BU701801	UI-M-FIO-	329	34.6	4.5	689	4	BI662480	BI662480 603304472
C 257	363	6	BD450685	B0264A02-	C 330	34.6	4.5	695	9	AG001435	AG001435 Homo sap1
C 258	391	5	BQ149628	NF107A11F	331	34.6	4.5	707	8	BH980005	BH980005 Odf10E07
C 259	426	7	CG699164	E0417G08-	332	34.6	4.5	712	4	BG863366	BG863366 602797005
C 260	439	7	CF903111	A040OC09-	C 333	34.6	4.5	722	5	BP461634	BP461634 602797005
C 261	442	8	B78782	CIT-HSP-616	334	34.6	4.5	723	5	EX309208	EX309208 BX309208
C 262	480	6	CF168185	B079SF09-	335	34.6	4.5	729	5	BQ580323	BQ580323 ACB89-jml
C 263	487	6	CF167827	B079DF04-	336	34.6	4.5	735	4	BI656976	BI656976 603284594
C 264	500	6	CA557216	K022AA09-	337	34.6	4.5	735	5	EX746817	EX746817 BX746817
C 265	501	9	CL721921	OR.BBa005	C 338	34.6	4.5	738	5	BP459092	BP459092 BP459092
C 266	502	7	CK933020	K0853B08-	339	34.6	4.5	741	4	BI853687	BI853687 603380827
C 267	508	7	CN705083	E049SF08-	340	34.6	4.5	755	4	BG975001	BG975001 602843412
C 268	510	7	CN667348	A0853C07-	341	34.6	4.5	755	9	CE218122	CE218122 tigr-g88-
C 269	512	6	CD538284	B0201G09-	342	34.6	4.5	756	9	CC568180	CC568180 CH240.442
C 270	517	7	CF700974	E0443C08-	343	34.6	4.5	756	9	BI657811	BI657811 603283320
C 271	519	2	BF113440	EST441030	344	34.6	4.5	760	4	BI657811	BI657811 603283320
C 272	522	6	CF167867	B0791B07-	345	34.6	4.5	770	4	BI656261	BI656261 603283049
C 273	523	7	CN692328	E0321D05-	346	34.6	4.5	778	4	BG861708	BG861708 602795292
C 274	530	6	CD546447	B0274B05-	C 347	34.6	4.5	782	7	CNS20527	CNS20527 GQ0107.B3
C 275	533	7	CN692711	E0326G01-	348	34.6	4.5	788	4	BI654515	BI654515 603281901
C 276	543	5	BQ835038	PO ad 06E	349	34.6	4.5	800	4	BI655730	BI655730 603281325
C 277	550	7	CN696471	E0379H04	350	34.6	4.5	821	4	BI655297	BI655297 603283320
C 278	553	6	CF164817	B0748C03-	351	34.6	4.5	853	4	BI657228	BI657228 603282904
C 279	606	7	CO118046	GR.EB020	352	34.6	4.5	877	8	AQ856793	AQ856793 nbeeb0004K
C 280	608	5	BQ560211	H4062H10-	C 353	34.6	4.5	904	9	CC872533	CC872533 NDL.118B2
C 281	625	7	CF915409	B0979D07-	354	34.6	4.5	908	4	BI655773	BI655773 603281375
C 282	641	7	CF915058	B0973E03-	355	34.6	4.5	925	9	CNS04KMP	AL295018 Tetraodon
C 283	657	7	CK390520	K0820A11-	356	34.6	4.5	1000	4	BI656544	BI656544 603285987
C 284	668	7	CK392685	K0848G06-	357	34.6	4.5	1101	9	CNS0100X	AL098379 Drocephal
C 285	671	5	BQ745402	UI-M-EW0-	358	34.6	4.5	1103	4	BG861866	BG861866 602794817
C 286	686	7	CK633779	UI-M-HN0-	C 359	34.6	4.5	256	1	AV276642	AV276642 AV276642
C 287	689	1	AV385901	AV385901	C 360	34.4	4.5	265	7	CF612604	CF612604 lael13C11
C 288	691	7	CB244780	UI-M-HN0-	C 361	34.4	4.5	266	7	CF352876	CF352876 lab50G07
C 289	693	6	CB244551	UI-M-FY0-	C 362	34.4	4.5	266	7	CF755092	CF755092 lae52h12
C 290	694	7	CNS17967	UI-M-HS0-	C 363	34.4	4.5	267	7	CF968907	CF968907 laq74e08
C 291	706	5	BM964142	UI-M-EQ0-	C 364	34.4	4.5	279	7	CK384136	CK384136 lah02H05
C 292	715	6	CB245343	UI-M-FY0-	C 365	34.4	4.5	280	7	CF612108	CF612108 lae28a03
C 293	722	6	CB525667	UI-M-FY0-	C 366	34.4	4.5	283	7	CF352989	CF352989 lab60C04
C 294	732	7	CK639584	UI-M-HN0-	C 367	34.4	4.5	285	7	CK374159	CK374159 la157d10
C 295	739	6	CB521908	UI-M-GH0-	C 368	34.4	4.5	286	2	BB090521	BB090521 BB090521
C 296	742	6	CB244185	UI-M-FY0-	C 369	34.4	4.5	287	2	BB141202	BB141202 BB141202
C 297	751	7	CK635957	UI-M-HN0-	C 370	34.4	4.5	288	7	CF545042	CF545042 lad86h01
C 298	751	7	CO101715	GR.EB002	C 371	34.4	4.5	289	5	BX254614	BX254614 BX254614
C 299	755	9	CNS020HE	Tetraodon	C 372	34.4	4.5	297	2	BB025145	BB025145 BB025145
C 300	771	6	CA761866	GR.Bb002	C 373	34.4	4.5	299	2	BB366155	BB366155 BB366155
C 301	772	6	CA764724	AF53-Rpf	C 374	34.4	4.5	300	2	BB211801	BB211801 BB211801
C 302	775	7	CO086468	GR.Ea04H	C 375	34.4	4.5	300	2	BB298714	BB298714 BB298714
C 303	789	7	CF668769	RFCNT1.38	C 376	34.4	4.5	301	1	AV347881	AV347881 AV347881
C 304	815	6	CB244766	UI-M-FY0-	C 377	34.4	4.5	305	1	AV348624	AV348624 AV348624
C 305	823	7	CNS15568	UI-M-HQ0-	C 378	34.4	4.5	322	1	AV318704	AV318704 AV318704
C 306	853	8	BH584567	BOGFV09TR	C 379	34.4	4.5	323	2	BB070791	BB070791 BB070791
C 307	865	8	BZ172638	CH230-369	C 380	34.4	4.5	329	2	BE956586	BE956586 UI-M-BG2-
C 308	878	6	CB208450	AGENCOURT	C 381	34.4	4.5	330	2	AW121527	AW121527 UI-M-BH2
C 309	885	4	BI656076	603284735	C 382	34.4	4.5	331	2	BB392044	BB392044 BB392044
C 310	942	9	CNS022394	Tetraodon	C 383	34.4	4.5	332	2	BB793509	BB793509 BB793509
C 311	978	3	CR713554	Tetraodon	C 384	34.4	4.5	350	2	AW240480	AW240480 ug35d07.x
C 312	1098	9	CNS92661	ZMWBC054	C 385	34.4	4.5	379	2	BB738128	BB738128 BB738128
C 313	1130	9	CC932661	CC932661	C 386	34.4	4.5	382	2	BB738074	BB738074 BB738074
C 314	1233	6	CD699634	EST16030	C 387	34.4	4.5	382	7	CK377808	CK377808 la108g10
C 315	394	8	AQ241575	CITBI-EI-	C 388	34.4	4.5	387	4	BM124429	BM124429 L0539H12-
C 316	430	7	CO722365	Mdfr3019n	C 389	34.4	4.5	393	6	BY642121	BY642121 BY642121

C 390	34.4	4.5	419	2	BB742345	BB742345	C 463	34.2	4.5	552	6	CA016927	CA016927
C 391	34.4	4.5	423	6	BB826487	BB826487	C 464	34.2	4.5	563	9	CE461481	CE461481
C 392	34.4	4.5	429	6	CA876962	K0952B01-	C 465	34.2	4.5	637	9	AG014550	AG014550
C 393	34.4	4.5	439	4	B7065493	B7065493	C 466	34.2	4.5	655	7	CLN135161	CLN135161
C 394	34.4	4.5	451	2	BB770395	BB770395	C 467	34.2	4.5	660	9	CL750932	CL750932
C 395	34.4	4.5	457	1	AI118573	AI118573	C 468	34.2	4.5	672	6	CD394634	CD394634
C 396	34.4	4.5	457	5	BF755914	BF755914	C 469	34.2	4.5	694	1	AV920760	AV920760
C 397	34.4	4.5	458	6	CD710397	CD710397	C 470	34.2	4.5	696	4	BJ734675	BJ734675
C 398	34.4	4.5	465	2	BB744930	BB744930	C 471	34.2	4.5	700	2	BE876198	BE876198
C 399	34.4	4.5	472	4	BM146485	BM146485	C 472	34.2	4.5	716	8	BH110294	BH110294
C 400	34.4	4.5	472	8	QA0479756	QA0479756	C 473	34.2	4.5	726	6	BY765148	BY765148
C 401	34.4	4.5	478	2	BB829859	BB829859	C 474	34.2	4.5	733	6	CF270923	CF270923
C 402	34.4	4.5	483	1	AI315295	AI315295	C 475	34.2	4.5	741	9	EX142905	EX142905
C 403	34.4	4.5	487	1	BB762298	BB762298	C 476	34.2	4.5	743	7	CF391770	CF391770
C 404	34.4	4.5	498	1	AI957077	AI957077	C 477	34.2	4.5	788	7	CF391770	CF391770
C 405	34.4	4.5	499	8	A2517364	A2517364	C 478	34.2	4.5	799	9	CG812405	CG812405
C 406	34.4	4.5	500	2	AW763553	AW763553	C 479	34.2	4.5	833	9	CL671547	CL671547
C 407	34.4	4.5	500	2	BF017898	BF017898	C 480	34.2	4.5	834	2	BF675136	BF675136
C 408	34.4	4.5	508	2	AW610767	AW610767	C 481	34.2	4.5	840	8	BZ816570	BZ816570
C 409	34.4	4.5	508	6	CD540697	CD540697	C 482	34.2	4.5	883	9	CG464206	CG464206
C 410	34.4	4.5	510	1	AI461967	AI461967	C 483	34.2	4.5	939	9	CL470056	CL470056
C 411	34.4	4.5	514	2	BB763133	BB763133	C 484	34.2	4.5	1018	8	CG255799	CG255799
C 412	34.4	4.5	514	2	BB764583	BB764583	C 485	34.2	4.5	1558	3	CNS0A9EJ	CNS0A9EJ
C 413	34.4	4.5	516	5	BA665523	BA665523	C 486	34.2	4.5	1558	3	AI835944	AI835944
C 414	34.4	4.5	523	6	CD707517	CD707517	C 487	34.2	4.5	324	1	AI835944	AI835944
C 415	34.4	4.5	525	2	BB764443	BB764443	C 488	34.2	4.5	409	8	AZ004640	AZ004640
C 416	34.4	4.5	532	2	BB769183	BB769183	C 489	34.2	4.5	414	8	AZ094701	AZ094701
C 417	34.4	4.5	534	2	BB768928	BB768928	C 490	34.2	4.5	493	8	AZ410718	AZ410718
C 418	34.4	4.5	563	4	B1105752	B1105752	C 491	34.2	4.5	516	5	BU476821	BU476821
C 419	34.4	4.5	576	5	BF768948	BF768948	C 492	34.2	4.5	517	5	BU476821	BU476821
C 420	34.4	4.5	582	4	CD684058	CD684058	C 493	34.2	4.5	526	8	CC410978	CC410978
C 421	34.4	4.5	582	6	CD684058	CD684058	C 494	34.2	4.5	536	5	BU496612	BU496612
C 422	34.4	4.5	583	5	CG952461	CG952461	C 495	34.2	4.5	593	2	AW533498	AW533498
C 423	34.4	4.5	587	9	BB768864	BB768864	C 496	34.2	4.5	604	5	BU495658	BU495658
C 424	34.4	4.5	589	5	BB768864	BB768864	C 497	34.2	4.5	604	5	BU495658	BU495658
C 425	34.4	4.5	597	5	BB757053	BB757053	C 498	34.2	4.5	611	7	CNS38312	CNS38312
C 426	34.4	4.5	603	8	AQ459573	AQ459573	C 499	34.2	4.5	611	7	CNS38312	CNS38312
C 427	34.4	4.5	605	4	BI477202	BI477202	C 500	34.2	4.5	623	1	AI057980	AI057980
C 428	34.4	4.5	611	5	BY479578	BY479578	C 501	34.2	4.5	623	1	AI057980	AI057980
C 429	34.4	4.5	620	6	CD690618	CD690618	C 502	34.2	4.5	631	8	AZ467632	AZ467632
C 430	34.4	4.5	623	6	CD683742	CD683742	C 503	34.2	4.5	631	8	AZ467632	AZ467632
C 431	34.4	4.5	647	4	BU065840	BU065840	C 504	34.2	4.5	647	9	CG945014	CG945014
C 432	34.4	4.5	647	6	CB507035	CB507035	C 505	34.2	4.5	655	8	BH882460	BH882460
C 433	34.4	4.5	689	8	BH945418	BH945418	C 506	34.2	4.5	661	8	BH882460	BH882460
C 434	34.4	4.5	694	8	AZ869901	AZ869901	C 507	34.2	4.5	670	8	BZ324568	BZ324568
C 435	34.4	4.5	717	5	BZ203953	BZ203953	C 508	34.2	4.5	674	8	BZ324568	BZ324568
C 436	34.4	4.5	724	6	CF283043	CF283043	C 509	34.2	4.5	674	8	BZ324568	BZ324568
C 437	34.4	4.5	735	8	BB057573	BB057573	C 510	34.2	4.5	687	4	CG128443	CG128443
C 438	34.4	4.5	774	9	CR079959	CR079959	C 511	34.2	4.5	688	4	CG128443	CG128443
C 439	34.4	4.5	846	7	CF836623	CF836623	C 512	34.2	4.5	698	9	CR033761	CR033761
C 440	34.4	4.5	897	7	CF798587	CF798587	C 513	34.2	4.5	715	7	CNS38407	CNS38407
C 441	34.4	4.5	902	6	CB198161	CB198161	C 514	34.2	4.5	719	9	AG137836	AG137836
C 442	34.4	4.5	909	8	AF011186	AF011186	C 515	34.2	4.5	755	8	BZ620740	BZ620740
C 443	34.4	4.5	915	9	CL040341	CL040341	C 516	34.2	4.5	769	9	AG184404	AG184404
C 444	34.4	4.5	946	9	CL016927	CL016927	C 517	34.2	4.5	769	9	AG184404	AG184404
C 445	34.4	4.5	970	9	CNS02KTM	CNS02KTM	C 518	34.2	4.5	804	7	CNS054476	CNS054476
C 446	34.4	4.5	1010	9	CL039923	CL039923	C 519	34.2	4.5	826	8	BZ222801	BZ222801
C 447	34.4	4.5	1028	9	CL034284	CL034284	C 520	34.2	4.5	893	5	BQ222536	BQ222536
C 448	34.4	4.5	1045	9	CL079107	CL079107	C 521	34.2	4.5	919	8	AZ545468	AZ545468
C 449	34.4	4.5	1050	9	CNS04EAX	CNS04EAX	C 522	34.2	4.5	995	9	CNS016WR	CNS016WR
C 450	34.4	4.5	1057	9	CL029984	CL029984	C 523	34.2	4.5	1051	8	CC246743	CC246743
C 451	34.4	4.5	1064	9	CL034555	CL034555	C 524	34.2	4.5	1058	9	CNS04TN2	CNS04TN2
C 452	34.4	4.5	1086	9	CL016831	CL016831	C 525	34.2	4.5	1102	9	CNS01521	CNS01521
C 453	34.4	4.5	1196	9	CL104968	CL104968	C 526	34.2	4.5	338	1	AI724183	AI724183
C 454	34.2	4.5	275	2	BE702156	BE702156	C 527	33.8	4.4	349	6	CA770616	CA770616
C 455	34.2	4.5	275	4	BI962355	BI962355	C 528	33.8	4.4	356	1	AU276935	AU276935
C 456	34.2	4.5	401	8	AZ226964	AZ226964	C 529	33.8	4.4	425	5	BX721215	BX721215
C 457	34.2	4.5	450	5	BB128791	BB128791	C 530	33.8	4.4	434	4	BI746750	BI746750
C 458	34.2	4.5	453	1	AA733437	AA733437	C 531	33.8	4.4	477	8	AQ642250	AQ642250
C 459	34.2	4.5	503	4	BJ467184	BJ467184	C 532	33.8	4.4	480	8	AQ053239	AQ053239
C 460	34.2	4.5	513	5	BP656183	BP656183	C 533	33.8	4.4	488	9	CR499096	CR499096
C 461	34.2	4.5	534	4	BJ467249	BJ467249	C 534	33.8	4.4	488	5	BU813635	BU813635
C 462	34.2	4.5	549	9	CL312916	CL312916	C 535	33.8	4.4	513	8	BZ870333	BZ870333

C 536	33.8	4.4	532	8	AQ336448	HS_5017_B	C 609	33.6	4.4	835	7	CK090795	F025P39.3
C 537	33.8	4.4	538	9	TA200FF1Q	AL479212 T. brucei	610	33.6	4.4	966	5	BX377559	BX377559
C 538	33.8	4.4	555	1	A0067999	AI067999 EST209688	611	33.6	4.4	1020	5	BU541791	AGENCYCOURT
C 539	33.8	4.4	561	4	BJ222730	BJ222730	C 612	33.4	4.4	290	2	BB040102	BB040102
C 540	33.8	4.4	602	8	BH032088	BH032088 RPCI-24-3	C 613	33.4	4.4	436	9	FR0015156	F. rubripes
C 541	33.8	4.4	648	2	AW375610	AW375610 QVO-C7017	C 614	33.4	4.4	527	9	CG410561	gbs3 VM7
C 542	33.8	4.4	648	2	AW498070	AW498070 660041C04	C 615	33.4	4.4	547	4	BM432826	1J5U6810
C 543	33.8	4.4	649	1	AJ0803785	AJ0803785	C 616	33.4	4.4	548	7	CR573062	CR573062
C 544	33.8	4.4	653	1	AI067214	AI067214 EST208888	C 617	33.4	4.4	551	6	CB470264	en19 G06
C 545	33.8	4.4	663	9	CG954848	CG954848 MBEAM41TF	C 618	33.4	4.4	551	6	CH301028	CH230-179
C 546	33.8	4.4	672	1	AJ0803102	AJ0803102	C 619	33.4	4.4	564	8	AZ371157	LM0122B04
C 547	33.8	4.4	672	1	AJ0803102	AJ0803102	C 620	33.4	4.4	573	8	AZ371157	LM0122B04
C 548	33.8	4.4	676	9	CL133990	CL133990 mch2-130N	C 621	33.4	4.4	579	1	AU238264	AU238264
C 549	33.8	4.4	685	5	BU813117	BU813117 N005E02 P	C 622	33.4	4.4	587	8	AZ948037	2M0210022
C 550	33.8	4.4	703	7	CH853978	CH853978 Ha mx0.19	C 623	33.4	4.4	593	7	CN247408	EST013300
C 551	33.8	4.4	711	7	CF478402	CF478402 RTW3_18	C 624	33.4	4.4	604	6	CA728754	wd11C.pk0
C 552	33.8	4.4	726	5	BU884566	BU884566 R012D07 P	C 625	33.4	4.4	604	7	CN878644	CN878644
C 553	33.8	4.4	729	9	CK109741	CK109741 N021B05 P	C 626	33.4	4.4	613	9	CL579090	OB BA003
C 554	33.8	4.4	738	6	CB311718	CB311718 AGENCYCOURT	C 627	33.4	4.4	626	8	AQ377603	RPCI11-14
C 555	33.8	4.4	742	6	CA057347	CA057347 sealrgp53	C 628	33.4	4.4	629	9	CNS05K0K	Tetraodon
C 556	33.8	4.4	747	9	CNS00922	AL054517 Drosophila	C 629	33.4	4.4	646	8	BH270084	CH230-6N1
C 557	33.8	4.4	755	7	CF923529	CF923529 ML MQ1 06	C 630	33.4	4.4	651	1	AJ789256	AJ789256
C 558	33.8	4.4	774	5	BM166560	BM166560	C 631	33.4	4.4	668	7	CO603742	DG8-26811
C 559	33.8	4.4	778	9	CR095245	CR095245 Reverse 8	C 632	33.4	4.4	670	1	AA020845	ze64a07.1
C 560	33.8	4.4	790	8	BH040645	BH040645 RPCI-24-3	C 633	33.4	4.4	692	1	AI729444	BNLCH133
C 561	33.8	4.4	809	8	BH575837	BH575837 BOGBQ82TF	C 634	33.4	4.4	718	8	BH926990	od121C10
C 562	33.8	4.4	837	5	BU812937	BU812937 N003B12 P	C 635	33.4	4.4	720	8	BH550487	BOHKS40TF
C 563	33.8	4.4	842	5	CO574783	CO574783 AGENCYCOURT	C 636	33.4	4.4	745	5	BX302265	BX302265
C 564	33.8	4.4	842	5	BM397496	BM397496 S009-0-33	C 637	33.4	4.4	755	8	AQ751371	HS 5575 B
C 565	33.8	4.4	845	7	CO199220	CO199220 G801_19_D	C 638	33.4	4.4	757	5	BU363716	603785288
C 566	33.8	4.4	856	7	CO198154	CO198154 G801_11_D	C 639	33.4	4.4	768	8	CC343736	OGUAP11TH
C 567	33.8	4.4	880	5	BX739977	BX739977 BX739973	C 640	33.4	4.4	799	7	CR563909	CR563909
C 568	33.8	4.4	881	5	BX739973	BX739973 BX739973	C 641	33.4	4.4	821	7	CR563909	CR563909
C 569	33.8	4.4	884	4	BG433065	BG433065 60246804	C 642	33.4	4.4	823	8	BZ746916	PUCEQ77TD
C 570	33.8	4.4	898	8	AZ528384	AZ528384 ENTBX21TR	C 643	33.4	4.4	848	5	BZ325524	603490628
C 571	33.8	4.4	904	8	AZ546660	AZ546660 ENTFQ22TF	C 644	33.4	4.4	859	8	BU325524	603490628
C 572	33.8	4.4	904	8	AZ546660	AZ546660 ENTFQ22TF	C 645	33.4	4.4	871	8	BH159288	ENTSB26TF
C 573	33.8	4.4	905	9	CG919472	CG919472 Drosophila	C 646	33.4	4.4	893	8	AZ687955	ENTHPS5TF
C 574	33.8	4.4	914	9	CG919472	CG919472 MBEMJ54TR	C 647	33.4	4.4	894	8	AZ547012	ENTHPS5TF
C 575	33.8	4.4	942	8	BH157632	BH157632 ENTSV32TF	C 648	33.4	4.4	895	8	BH146492	ENTHPS5TF
C 576	33.8	4.4	973	8	AZ670650	AZ670650 ENTHC61TF	C 649	33.4	4.4	908	4	BG295613	602392995
C 577	33.8	4.4	1101	9	CNS00FVE	AL071298 Drosophila	C 650	33.4	4.4	918	8	AZ139584	SP_0158A
C 578	33.6	4.4	202	6	CA317230	CA317230 UI-M-FW0-	C 651	33.4	4.4	924	8	AZ674562	ENT116TF
C 579	33.6	4.4	279	2	BE058564	BE058564 sn17909.Y	C 652	33.4	4.4	931	5	BQ734031	AGENCYCOURT
C 580	33.6	4.4	328	1	AU261705	AU261705 AU261705	C 653	33.4	4.4	1101	9	CNS0039G	AL063921 Drosophila
C 581	33.6	4.4	354	5	BQ602703	BQ602703 MI-P-NA-a	C 654	33.4	4.4	1273	9	CNS027009	CH216-24M
C 582	33.6	4.4	395	5	BP633395	BP633395 BP633395	C 655	33.4	4.4	1273	9	CNS027009	CH216-24M
C 583	33.6	4.4	405	5	BP660013	BP660013 BP660013	C 656	33.4	4.4	1534	3	CNS0A9W8	EX819392 Arabidops
C 584	33.6	4.4	412	8	BZ671900	BZ671900 PUBIC31TD	C 657	33.4	4.4	1568	8	CC190488	AT261-191
C 585	33.6	4.4	422	5	BU031097	BU031097 QHJ17G20	C 658	33.2	4.3	244	4	BG231287	hah4908
C 586	33.6	4.4	451	8	BH491945	BH491945 BOHMR03TF	C 659	33.2	4.3	246	4	BG231287	hah4908
C 587	33.6	4.4	473	8	AZ518814	AZ518814 RPCI-11-3	C 660	33.2	4.3	287	2	BB285429	BB285429
C 588	33.6	4.4	482	8	AQ129455	AQ129455 HS 3045 A	C 661	33.2	4.3	302	4	BM535932	BM535932
C 589	33.6	4.4	500	7	CP405836	CP405836 CSECS05H	C 662	33.2	4.3	319	9	CE199185	CE199185 tigr-g88-
C 590	33.6	4.4	503	5	BQ602443	BQ602443 MI-P-NA-a	C 663	33.2	4.3	358	4	BG098618	BG098618
C 591	33.6	4.4	547	8	AQ782708	AQ782708 HS 5327 A	C 664	33.2	4.3	368	7	CK714755	LECAD01B1
C 592	33.6	4.4	552	7	CK572012	CK572012 est_1 van	C 665	33.2	4.3	371	4	BM413609	EST587936
C 593	33.6	4.4	568	6	CB982247	CB982247 CAB7006	C 666	33.2	4.3	379	5	BM115736	BX115736
C 594	33.6	4.4	591	4	BH181221	BH181221 BOMK04TF	C 667	33.2	4.3	387	1	AI778135	EST259014
C 595	33.6	4.4	594	8	BH719437	BH719437 BOMK04TF	C 668	33.2	4.3	441	2	BB834287	BB834287
C 596	33.6	4.4	611	6	CF213145	CF213145 CFP100063	C 669	33.2	4.3	447	2	BB834287	BB834287
C 597	33.6	4.4	626	6	CD980922	CD980922 QAI18e02	C 670	33.2	4.3	450	7	CR291575	CR291575
C 598	33.6	4.4	648	9	AG071384	AG071384 Pan trogl	C 671	33.2	4.3	454	5	BY508612	BY508612
C 599	33.6	4.4	663	8	BH177905	BH177905 O10 D 16-	C 672	33.2	4.3	460	5	BP581349	BP581349
C 600	33.6	4.4	663	9	CNS07KCC	AL614862 T3 end of	C 673	33.2	4.3	468	1	AI778372	EST259251
C 601	33.6	4.4	686	8	BZ088224	BZ088224 lxx7ra03	C 674	33.2	4.3	477	2	BB434470	BB434470
C 602	33.6	4.4	696	6	CB290690	CB290690 UCRCS01_0	C 675	33.2	4.3	500	6	CF163019	BO719H05-
C 603	33.6	4.4	696	6	CD648250	CD648250 AUF 102 E	C 676	33.2	4.3	502	2	AW092191	EST285287
C 604	33.6	4.4	724	9	CNS00DLE	AL071881 Drosophila	C 677	33.2	4.3	503	6	CD552363	B0341F01-
C 605	33.6	4.4	726	9	CE455490	CE455490 tigr-g88-	C 678	33.2	4.3	510	7	CN683194	B0175D01-
C 606	33.6	4.4	741	4	BG696490	BG696490 602658810	C 679	33.2	4.3	518	6	CF165485	E0757D01-
C 607	33.6	4.4	780	9	CC872657	CC872657 NDL.22E13	C 680	33.2	4.3	519	8	AQ378907	RPCI11-16
C 608	33.6	4.4	824	8	BH354356	BH354356 CH230-221	C 681	33.2	4.3	521	6	CD554959	BO384F05-

C 682	33.2	4.3	522	6	CA870580	K0903B09-	C 755	33	4.3	578	5	BU629298	UI-H-FLO-
C 683	33.2	4.3	522	6	CA875662	K0942F11-	756	33	4.3	588	4	BU053905	BJ053905
C 684	33.2	4.3	530	4	BM413561	EST587888	C 757	33	4.3	589	7	CN633459	taf11b02.
C 685	33.2	4.3	533	7	CN673974	A0942C06-	758	33	4.3	591	7	CO636433	USDA-FP.1
C 686	33.2	4.3	534	5	BQ167571	WH00076 F	759	33	4.3	592	6	CF195241	USDA-FP.1
C 687	33.2	4.3	535	7	CN681771	E0155A06-	760	33	4.3	595	7	CF916477	B0995F05-
C 688	33.2	4.3	547	2	AW035331	EST280694	C 761	33	4.3	607	7	CO755397	Mdfct3049
C 689	33.2	4.3	559	7	CN690119	E0289A03-	762	33	4.3	610	7	CN633206	taf11b02.
C 690	33.2	4.3	574	8	AQ885296	HS.5522 B	763	33	4.3	631	5	BQ535624	STEM2.16-
C 691	33.2	4.3	577	1	AT895551	EST264954	C 764	33	4.3	634	1	AL714497	AL714497
C 692	33.2	4.3	579	2	BF098441	EST428962	C 765	33	4.3	638	5	BU673239	NL.12.78
C 693	33.2	4.3	579	4	BI993480	BI993480	766	33	4.3	640	7	CF915804	B0957H11-
C 694	33.2	4.3	591	9	CE175633	t1gr-g88-	767	33	4.3	640	7	CF915804	B0957H11-
C 695	33.2	4.3	594	8	AQ026573	CIT-HSP-2	C 768	33	4.3	647	5	BQ594695	E017404-0
C 696	33.2	4.3	598	4	BM409794	EST584121	769	33	4.3	666	6	CF173148	B0919C08-
C 697	33.2	4.3	603	7	CN353420	CN353420	C 770	33	4.3	671	1	AL642221	AL642221
C 698	33.2	4.3	612	6	CA875331	K0939C02-	771	33	4.3	672	2	AW979365	EST310413
C 699	33.2	4.3	617	9	CE202502	t1gr-g88-	772	33	4.3	676	8	BH956763	odh04d12.
C 700	33.2	4.3	619	2	AW934247	EST360090	773	33	4.3	677	2	BE613669	601504464
C 701	33.2	4.3	635	4	BQ097618	EST462137	C 774	33	4.3	683	9	CL599760	OB_Ba006
C 702	33.2	4.3	642	6	CF308048	ABF--01-L	C 775	33	4.3	691	5	BQ007955	UI-H-EIO-
C 703	33.2	4.3	646	6	CA879767	K0976F07-	C 776	33	4.3	693	9	CL814014	OR_CBa003
C 704	33.2	4.3	647	9	CR299014	Medicago	777	33	4.3	696	6	CB528171	UI-M-FYO-
C 705	33.2	4.3	660	4	BI935955	EST555844	C 778	33	4.3	696	8	AQ255734	nbx50014C
C 706	33.2	4.3	660	8	AQ252538	243PBEO4	779	33	4.3	701	1	AV783773	AV783773
C 707	33.2	4.3	664	8	AQ380827	RPC111-16	C 780	33	4.3	701	9	AG339045	Mus muscu
C 708	33.2	4.3	669	9	AG154904	Pan trogl	781	33	4.3	702	8	BH736306	BH736306
C 709	33.2	4.3	679	2	AW442803	EST307733	782	33	4.3	705	4	BG603336	EST502426
C 710	33.2	4.3	679	9	CL765303	OR_BBA013	783	33	4.3	705	4	BM674718	UI-B-EJO-
C 711	33.2	4.3	685	9	CE048480	t1gr-g88-	784	33	4.3	712	4	BZ074959	1kg38f06.
C 712	33.2	4.3	700	9	AG001434	Homo sapi	785	33	4.3	715	4	BI662482	603304474
C 713	33.2	4.3	701	7	CN754130	ID0AAA12A	C 786	33	4.3	733	8	BZ361823	1e25904.1b
C 714	33.2	4.3	731	9	CA485180	CH240.314	787	33	4.3	739	4	BG862087	602795622
C 715	33.2	4.3	779	9	CO750477	HS.5576 B	788	33	4.3	771	4	BI661001	603304092
C 716	33.2	4.3	791	4	BI105506	602891839	789	33	4.3	774	5	BU316793	603855209
C 717	33.2	4.3	795	4	BG889180	EST515031	C 790	33	4.3	788	6	CD906120	G468.103P
C 718	33.2	4.3	803	5	BG233923	603411828	792	33	4.3	790	9	CL554281	OB_Ba000
C 719	33.2	4.3	809	9	CG962465	MBENH21TF	C 793	33	4.3	811	7	BZ428278	RBNM31TR
C 720	33.2	4.3	817	4	BM410777	EST585104	C 794	33	4.3	814	8	BZ110323	CH230-230
C 721	33.2	4.3	894	7	CK796769	AGENCOURT	C 795	33	4.3	820	9	CNS0230Z	Tetraodon
C 722	33.2	4.3	903	9	CNS06X04	AL419114	796	33	4.3	821	8	BH678554	BOHYU16TR
C 723	33.2	4.3	920	7	CK263090	EST709168	797	33	4.3	832	7	CO580772	ILLUMIGEN
C 724	33.2	4.3	956	5	BQ945685	AGENCOURT	C 798	33	4.3	839	8	BZ519182	BOMR578TR
C 725	33.2	4.3	1115	8	CG300704	CH261-68L	C 799	33	4.3	846	9	CL839176	OR_CBa006
C 726	33.2	4.3	1319	9	CG745602	P038-3-C1	C 800	33	4.3	874	7	CN329377	Reverse s
C 727	33	33	173	9	CL002188	02S0069-0	C 801	33	4.3	865	9	CR258613	CR258613
C 728	33	33	232	5	BO156654	NF095B08I	C 802	33	4.3	874	7	BI654649	603285564
C 729	33	33	240	2	BB107987	BB107987	C 803	33	4.3	900	4	BI654649	603285564
C 730	33	33	249	1	AI864971	wk06b03.x	C 804	33	4.3	913	6	CB229507	AGENCOURT
C 731	33	33	295	5	BU618324	UI-H-FH1-	C 805	33	4.3	913	9	CNS0611Q	T7 end of
C 732	33	33	418	1	AV788577	AV788577	C 806	33	4.3	931	5	BH146438	ENTPR40TF
C 733	33	33	427	8	BZ768512	SALK.1403	C 807	33	4.3	966	2	BQ885412	AGENCOURT
C 734	33	33	434	1	AT752199	cn14C06.Y	C 808	33	4.3	977	4	BI559237	602030858
C 735	33	33	462	8	BH706749	BOMDH80TR	C 809	33	4.3	1029	1	AL573715	603240863
C 736	33	33	480	8	BH440195	BOGINS7TF	C 810	33	4.3	1071	9	CNS057KE	Tetraodon
C 737	33	33	490	7	CN551520	ta073h06.	C 811	33	4.3	1117	8	CC216496	CH261-781
C 738	33	33	494	2	AW410218	fh05c12.Y	C 812	33	4.3	1200	9	CNS016CI	AL106572
C 739	33	33	495	2	AW410218	fh05c12.Y	C 813	33	4.3	1212	8	BZ691036	Drosophila
C 740	33	33	508	7	CO644367	USDA-FP.1	C 814	33	4.3	1389	9	CG751034	SP_Ba000
C 741	33	33	511	7	CNS58588	ta073h06.	C 815	33	4.3	1871	3	BG2751034	Arabidops
C 742	33	33	511	7	N37165	18375 Lambd	C 816	33	4.3	2001	3	CNS042XR	BC015705
C 743	33	33	518	9	CE022124	t1gr-g88-	C 817	32.8	4.3	213	7	CF371656	CF371656
C 744	33	33	521	5	BU895718	X030A07 P	C 818	32.8	4.3	244	1	AV360468	AV360468
C 745	33	33	522	8	B83744	CpG0094A Cp	C 819	32.8	4.3	245	1	AV315185	AV315185
C 746	33	33	524	4	BI770986	603055323	C 820	32.8	4.3	249	2	BQ074609	BQ074609
C 747	33	33	525	5	BQ002597	UI-H-E11-	C 821	32.8	4.3	254	7	BB141111	BB141111
C 748	33	33	539	1	AL914516	AL914516	C 822	32.8	4.3	257	7	CF969459	lag68a09.
C 749	33	33	540	5	BU696710	LL2in1083	C 823	32.8	4.3	258	7	CF379612	lad06d07.
C 750	33	33	540	8	AQ680994	HS.5492 B	C 824	32.8	4.3	257	1	AV255530	AV255530
C 751	33	33	548	7	CF949646	UI-M-HK0-	C 825	32.8	4.3	280	2	AV052841	AV052841
C 752	33	33	558	9	CL554363	OB_Ba000	C 826	32.8	4.3	280	1	BB432211	BB432211
C 753	33	33	568	8	BZ904403	CH260.25P	C 827	32.8	4.3	285	7	CK372120	lai33h10.
C 754	33	33	576	4	BM669984	UI-B-DW1-							

C 828	32.8	4.3	294	2	BB026976	BB026976	901	32.8	4.3	896	9	CG929597	CG929597 MBBJP65TP
C 829	32.8	4.3	298	2	BB110605	BB110605	902	32.8	4.3	898	9	CG166446	CG166446 PUFQ92TB
C 830	32.8	4.3	299	2	BB124772	BB124772	C 903	32.8	4.3	911	9	CNS070R2	AL232972 T7 end of
C 831	32.8	4.3	303	2	BB221261	BB221261	C 904	32.8	4.3	914	8	AZ545365	AZ545365 ENTFF91TF
C 832	32.8	4.3	314	2	BB719396	BB719396	C 905	32.8	4.3	915	8	CNS02K1P	AL201552 Tetraodon
C 833	32.8	4.3	320	2	BB138492	BB138492	C 906	32.8	4.3	931	8	BH135538	BH135538 ENTOS03TF
C 834	32.8	4.3	337	2	BB125831	BB125831	C 907	32.8	4.3	942	9	AL086614	AL086614 T7 end of
C 835	32.8	4.3	346	4	EG406288	EG406288 sac29h02.	C 908	32.8	4.3	998	9	CL070481	CL070481 CH216-118
C 836	32.8	4.3	348	4	EG092709	EG092709 mac15h11.	C 909	32.8	4.3	1101	8	CNS016QS	CC297017 CH261-43H
C 837	32.8	4.3	357	2	BB745689	BB745689	C 910	32.8	4.3	1200	8	AG3340923	AG3340923 Mus muscu
C 838	32.8	4.3	373	1	AL385382	AL385382 MCB38C06	C 911	32.8	4.3	1214	9	AG3340923	AG3340923 Mus muscu
C 839	32.8	4.3	380	7	CF424488	CF424488 la3d31d05.	C 912	32.8	4.3	1219	9	AG3340923	AG3340923 Mus muscu
C 840	32.8	4.3	381	6	CA890445	CA890445 B015SD04.	C 913	32.8	4.3	1606	3	BC068017	BC068017 Homo sapi
C 841	32.8	4.3	382	1	AL385383	AL385383 MCB38C06	C 914	32.8	4.3	2148	3	AK035990	AK035990 Mus muscu
C 842	32.8	4.3	386	6	CD706108	CD706108 EST22635	C 915	32.6	4.3	225	4	BI691815	BI691815 G03307537
C 843	32.8	4.3	408	2	BF561593	BF561593 UI-R-C0-1	C 916	32.6	4.3	241	8	BZ523111	BZ523111 BOKAD78TR
C 844	32.8	4.3	414	1	AA710655	AA710655 vt43e10.r	C 917	32.6	4.3	261	4	BI038664	BI038664 IL3-NT028
C 845	32.8	4.3	414	2	BF387419	BF387419 UI-R-CAL-	C 918	32.6	4.3	261	4	BI039792	BI039792 IL3-NT028
C 846	32.8	4.3	426	2	AW013852	AW013852 UI-H-BIO-	C 919	32.6	4.3	269	2	BE240137	BE240137 EST404186
C 847	32.8	4.3	448	8	AQ870616	AQ870616 ndeb0040E	C 920	32.6	4.3	303	1	AI805603	AI805603 tx97b08.x
C 848	32.8	4.3	452	2	BB776148	BB776148	C 921	32.6	4.3	351	6	CB780941	CB780941 AMGNNUC:M
C 849	32.8	4.3	512	7	CF745811	CF745811 UI-M-GVO-	C 922	32.6	4.3	433	1	AL675598	AL675598 AL675598
C 850	32.8	4.3	518	5	BQ554425	BQ554425 H4028A11-	C 923	32.6	4.3	441	5	BQ321431	BQ321431 MR3-CT046
C 851	32.8	4.3	522	2	BB751730	BB751730	C 924	32.6	4.3	481	2	BE251135	BE251135 G01107196
C 852	32.8	4.3	541	7	CN681524	CN681524 E015AF11-	C 925	32.6	4.3	488	8	BH041279	BH041279 RPCI-24-3
C 853	32.8	4.3	541	7	CN686589	CN686589 R0227D11-	C 926	32.6	4.3	517	8	AQ510066	AQ510066 nxbx0094B
C 854	32.8	4.3	562	9	CL764258	CL764258 OR_BBa013	C 927	32.6	4.3	528	9	CES19937	CES19937 t1gr-g88
C 855	32.8	4.3	563	5	BQ398706	BQ398706 N15C_m010	C 928	32.6	4.3	538	5	BO198195	BO198195 NXLV126.H
C 856	32.8	4.3	572	2	BF358706	BF358706 MR1-ET000	C 929	32.6	4.3	544	8	AQ983337	AQ983337 RPCI-23-3
C 857	32.8	4.3	576	7	CF430166	CF430166 PH1_26_H0	C 930	32.6	4.3	555	8	BZ277916	BZ277916 CH230-156
C 858	32.8	4.3	577	6	CB442335	CB442335 632932_MA	C 931	32.6	4.3	558	8	B93214	B93214 CIT-HSP-217
C 859	32.8	4.3	587	6	CD153781	CD153781 ML1-0035T	C 932	32.6	4.3	566	5	BP764509	BP764509 BP764509
C 860	32.8	4.3	593	3	CN675335	CN675335 A0962A07-	C 933	32.6	4.3	574	4	AL671828	AL671828 df69a06.x
C 861	32.8	4.3	605	8	AZ092149	AZ092149 RPCI-23-4	C 934	32.6	4.3	578	1	AL722362	AL722362 AL722362
C 862	32.8	4.3	609	3	CL606970	CL606970 CH240_170	C 935	32.6	4.3	585	8	AZ320089	AZ320089 1M0039920
C 863	32.8	4.3	610	1	AI788741	AI788741 uX5308.x	C 936	32.6	4.3	590	7	CK3089573	CK3089573 C019P10.3
C 864	32.8	4.3	612	7	CF891779	CF891779 A0100H11-	C 937	32.6	4.3	594	8	BH769474	BH769474 BMBAC366A
C 865	32.8	4.3	612	9	CL712399	CL712399 OR_BBa003	C 938	32.6	4.3	595	8	BH869671	BH869671 h14e05.b
C 866	32.8	4.3	614	8	BH760525	BH760525 BMBAC313P	C 939	32.6	4.3	600	7	CO372163	CO372163 tah98A06.
C 867	32.8	4.3	621	4	BJ7111905	BJ7111905	C 940	32.6	4.3	630	1	AT003850	AT003850
C 868	32.8	4.3	631	5	BM991828	BM991828 UI-H-DFL-	C 941	32.6	4.3	650	2	BE427659	BE427659 PSR7312.I
C 869	32.8	4.3	635	4	EG443516	EG443516 GA_Ea002	C 942	32.6	4.3	658	2	AW684747	AW684747 NF021F05N
C 870	32.8	4.3	636	2	AW586848	AW586848 EST318471	C 943	32.6	4.3	688	7	CO176656	CO176656 NDL1_63_H
C 871	32.8	4.3	639	4	BJ264614	BJ264614	C 944	32.6	4.3	724	7	CN041380	CN041380 nm_40h_g5
C 872	32.8	4.3	642	7	CK315060	CK315060 SB020401A2	C 945	32.6	4.3	724	8	BG722129	BG722129 PUDAN39TF
C 873	32.8	4.3	660	9	CL757894	CL757894 OR_BBa012	C 946	32.6	4.3	727	4	BG723382	BG723382 602694045
C 874	32.8	4.3	665	8	AQ878469	AQ878469 HS_3081.A	C 947	32.6	4.3	729	7	CN531184	CN531184 UI-M-HQ0-
C 875	32.8	4.3	665	9	EX189742	EX189742 Danilo rer	C 948	32.6	4.3	740	1	AJ446279	AJ446279 AJ446279
C 876	32.8	4.3	678	7	CO682600	CO682600 DGL1-156F	C 949	32.6	4.3	746	5	BU121925	BU121925 603148640
C 877	32.8	4.3	680	2	BB127711	BB127711	C 950	32.6	4.3	746	9	CG252503	CG252503 OGIAR66TV
C 878	32.8	4.3	685	8	AQ322944	AQ322944 RPCI11-10	C 951	32.6	4.3	751	9	CR121431	CR121431 Reverse 8
C 879	32.8	4.3	686	5	BX112698	BX112698	C 952	32.6	4.3	751	9	CG252492	CG252492 OGIAR66TH
C 880	32.8	4.3	693	4	BI503838	BI503838 BB170026B	C 953	32.6	4.3	758	5	BU225465	BU225465 603398746
C 881	32.8	4.3	694	9	CL819689	CL819689 OR_CBa003	C 954	32.6	4.3	767	5	BP433918	BP433918 BP433918
C 882	32.8	4.3	706	4	BJ282350	BJ282350 BU282350	C 955	32.6	4.3	769	7	CO176746	CO176746 NDL1_63_H
C 883	32.8	4.3	717	9	CL596203	CL596203 OB_Ba005	C 956	32.6	4.3	775	2	BEG20997	BEG20997 601493580
C 884	32.8	4.3	723	8	BH521966	BH521966 B0GE127TF	C 957	32.6	4.3	780	4	BI251779	BI251779 602994285
C 885	32.8	4.3	727	8	BH035130	BH035130 RPCI-24-3	C 958	32.6	4.3	780	8	AQ349389	AQ349389 RPCI11-11
C 886	32.8	4.3	728	7	CK303096	CK303096 SB02017A2	C 959	32.6	4.3	790	5	BU207869	BU207869 603950035
C 887	32.8	4.3	730	8	AQ243297	AQ243297 HS_2060.B	C 960	32.6	4.3	796	4	EG780413	EG780413 SEAU0C000
C 888	32.8	4.3	741	8	BZ718947	BZ718947 PUCFY59TD	C 961	32.6	4.3	796	5	BP435042	BP435042 BP435042
C 889	32.8	4.3	747	8	BZ119136	BZ119136 CH230-523	C 962	32.6	4.3	810	8	BG673724	BG673724 tx81456.c
C 890	32.8	4.3	765	9	CC746447	CC746447 ZMMBB012	C 963	32.6	4.3	834	4	BG540058	BG540058 602568689
C 891	32.8	4.3	768	4	BJ726391	BJ726391	C 964	32.6	4.3	844	8	AZ687551	AZ687551 ENTL253TR
C 892	32.8	4.3	803	9	CC738931	CC738931 ZMMBB010	C 965	32.6	4.3	847	9	CG173767	CG173767 MBBDW26TF
C 893	32.8	4.3	808	9	EX196960	EX196960 Danilo rer	C 966	32.6	4.3	871	9	CG173767	CG173767 PUFV166TF
C 894	32.8	4.3	821	9	CNS0091A	AL053819 Drosophila	C 967	32.6	4.3	872	9	CG328446	CG328446 OGIAR66TH
C 895	32.8	4.3	865	6	CA106362	CA106362 SCQHR101	C 968	32.6	4.3	880	8	AQ750737	AQ750737 HS_5574.B
C 896	32.8	4.3	867	4	CK153073	CK153073 FGAS03162	C 969	32.6	4.3	895	9	AK0506WAS	AK0506WAS T3_end of
C 897	32.8	4.3	869	7	BG754409	BG754409 602710024	C 970	32.6	4.3	897	5	BU142210	BU142210 603135333
C 898	32.8	4.3	869	7	CF618170	CF618170 AGENCOURT	C 971	32.6	4.3	919	8	BZ722126	BZ722126 PUDAN39TB
C 899	32.8	4.3	872	7	CN756996	CN756996 ID0AAIAE	C 972	32.6	4.3	920	7	CK417925	CK417925 AUF_ipint
C 900	32.8	4.3	891	8	AZ541750	AZ541750 ENTEN7TF	C 973	32.6	4.3				

C 974	32.6	4.3	922	8	A901220	HS_2013_B	1047	32.4	4.2	685	4	BJ023215	BJ023215
C 975	32.6	4.3	931	1	AL580292	AL580292	1048	32.4	4.2	698	5	CL566362	OB_Ba003
C 976	32.6	4.3	931	8	AZ672194	ENTH57TF	1049	32.4	4.2	706	5	BU368687	603595693
C 977	32.6	4.3	931	9	CNS0378W	CG130069	1050	32.4	4.2	714	5	EX782077	EX782077
C 978	32.6	4.3	946	9	CG130069	PUPSN16TD	1051	32.4	4.2	716	7	CNS90843	TTE000119
C 979	32.6	4.3	954	7	CG130069	brain_EST	1052	32.4	4.2	717	5	BU212422	604157440
C 980	32.6	4.3	967	9	CG1018559	CH216-3L1	1053	32.4	4.2	720	5	BU020295	SJFAPH09
C 981	32.6	4.3	967	9	CG130068	PUPSN16TB	1054	32.4	4.2	721	5	CR229846	Reverse s
C 982	32.6	4.3	997	9	CG125118	ISB1-86H1	1055	32.4	4.2	737	8	BZ395777	ZMNB44TR
C 983	32.6	4.3	1009	9	AL408098	T3 end of	1056	32.4	4.2	740	9	CC835606	ZMNB44TR
C 984	32.6	4.3	1032	9	CNS06014	AL06193 Drosophil	1057	32.4	4.2	741	9	CNS06N4B	AL406305 T3 end of
C 985	32.6	4.3	1075	2	BE781356	BE781356 601467090	1058	32.4	4.2	748	9	AG486476	Mus muscu
C 986	32.6	4.3	1089	9	CNS051RV	AL339268 Tetraodon	1059	32.4	4.2	750	9	CR243525	Forward s
C 987	32.6	4.3	1095	8	CC290569	CH261-60H	1060	32.4	4.2	751	5	CL813059	OR_Cha002
C 988	32.6	4.3	1125	3	CR677068	Tetraodon	1061	32.4	4.2	753	5	BU393380	603111956
C 989	32.4	4.2	197	2	BE319519	BE319519 NF019D12R	1062	32.4	4.2	758	9	AG303296	Mus muscu
C 990	32.4	4.2	201	2	BE320839	BE320839 NF029A10R	1063	32.4	4.2	773	7	CNS324769	AGENCOURT
C 991	32.4	4.2	268	2	BE322551	BE322551 BB322551	1064	32.4	4.2	776	9	AG317067	Mus muscu
C 992	32.4	4.2	286	2	BE293022	BE293022 BB293022	1065	32.4	4.2	780	8	BH932802	ode98h01
C 993	32.4	4.2	288	2	BE486727	BE486727 BB486727	1066	32.4	4.2	783	5	BU388146	603861243
C 994	32.4	4.2	292	2	BE078719	BE078719 BB078719	1067	32.4	4.2	792	5	BU108701	BU108701 603111956
C 995	32.4	4.2	305	2	BE201683	BE201683 BB201683	1068	32.4	4.2	798	7	CF437909	EST674254
C 996	32.4	4.2	307	2	BE0881332	BE0881332 QVO-OT003	1069	32.4	4.2	808	9	CC587295	CH240_385
C 997	32.4	4.2	341	5	BE220133	BE220133 BY220133	1070	32.4	4.2	810	9	AG550293	Mus muscu
C 998	32.4	4.2	352	5	BE220208	BE220208 BY220208	1071	32.4	4.2	835	7	CK193798	CK193798 SP_0094_B
C 999	32.4	4.2	379	5	BE067490	BE067490 M100H03_P	1072	32.4	4.2	871	8	AZ167234	AZ167234 SP_0094_B
C 1000	32.4	4.2	391	1	BE588507	BE588507 nm74a08.s	1073	32.4	4.2	874	8	AZ538638	ENTES77TF
C 1001	32.4	4.2	393	1	BE078719	BE078719 BB078719	1074	32.4	4.2	880	9	AZ669779	ENTIQ53TR
C 1002	32.4	4.2	398	1	BE078719	BE078719 BB078719	1075	32.4	4.2	888	9	CG818280	SOYAQ80TV
C 1003	32.4	4.2	402	1	BE025092	BE025092 C0509D07-	1076	32.4	4.2	883	9	CC588285	CH240_386
C 1004	32.4	4.2	408	2	BE514048	BE514048 xt79d06.x	1077	32.4	4.2	903	9	CL122525	ISB1-82E1
C 1005	32.4	4.2	419	1	BE516786	BE516786 UI-R-YO-V	1078	32.4	4.2	905	9	CG962271	MBELJ64TR
C 1006	32.4	4.2	423	9	CR248031	CR248031 Forward s	1079	32.4	4.2	930	6	CNS02PYE	Tetraodon
C 1007	32.4	4.2	435	1	BE393260	BE393260 tg09d01.x	1080	32.4	4.2	939	9	CB203539	AGENCOURT
C 1008	32.4	4.2	441	9	BE034741	BE034741 RPTC11-11	1081	32.4	4.2	933	9	CK193798	CK193798 SP_0094_B
C 1009	32.4	4.2	446	9	BE049015	BE049015 Reverse s	1082	32.4	4.2	964	9	CNS07CYU	AL439804 T7 end of
C 1010	32.4	4.2	460	1	BE162982	BE162982 A028P25U	1083	32.4	4.2	1035	9	CL112104	ISB1-56G2
C 1011	32.4	4.2	470	2	BE672766	BE672766 7b76g05.x	1084	32.4	4.2	1082	9	CNS06RUX	AL412447 T3 end of
C 1012	32.4	4.2	477	7	CNS058883	CNS058883 Salamande	1085	32.4	4.2	1101	9	CNS002B4	AL062483 Drosophil
C 1013	32.4	4.2	489	1	BE0911609	BE0911609 AV911609	1086	32.4	4.2	1139	8	CC191358	CH261-40L
C 1014	32.4	4.2	493	7	BE0622815	BE0622815 tad91h09.	1087	32.4	4.2	1226	9	CC291618	CH261-61D
C 1015	32.4	4.2	493	7	BE0622815	BE0622815 tad91h09.	1088	32.4	4.2	1226	9	CG755657	P051-1-G1
C 1016	32.4	4.2	500	8	BE0382497	BE0382497 RPTC11-16	1089	32.4	4.2	1377	9	CG755657	P051-1-G1
C 1017	32.4	4.2	509	2	BE382994	BE382994 601298987	1090	32.4	4.2	1593	8	CC232487	CH261-183
C 1018	32.4	4.2	517	7	CG638752	CG638752 D06_E10_F	1091	32.4	4.2	3313	3	AK046411	Mus muscu
C 1019	32.4	4.2	521	9	AG262630	AG262630 Lotus cor	1092	32.4	4.2	173	7	CK398902	CK398902 AGENCOURT
C 1020	32.4	4.2	522	6	CG307052	CG307052 Str-Pu691.	1093	32.4	4.2	264	5	BE489946	BE489946 DKFZP6861
C 1021	32.4	4.2	545	4	BE316477	BE316477 947022R05	1094	32.4	4.2	347	7	CF968439	lag14h11.
C 1022	32.4	4.2	548	5	BE089708	BE089708 rcs1h10.Y	1095	32.4	4.2	358	6	CF228104	CF228104 PtaX0008
C 1023	32.4	4.2	549	4	BE348559	BE348559 MEST293-B	1096	32.4	4.2	367	2	BE237502	BE237502 146821 MA
C 1024	32.4	4.2	563	1	BE490157	BE490157 EST246749	1097	32.4	4.2	374	7	R08219	R08219 Yf18b04.r1
C 1025	32.4	4.2	563	2	BE288844	BE288844 601094216	1098	32.4	4.2	382	8	B72702	B72702 RPTC11-10B1
C 1026	32.4	4.2	565	4	BE084440	BE084440 H3100H08-	1099	32.4	4.2	383	6	CH105148	CH105148 K-EST0103
C 1027	32.4	4.2	588	6	CA927621	CA927621 MTU6TR.P1	1100	32.4	4.2	386	9	CF480030	CF480030 Medicago
C 1028	32.4	4.2	589	9	CL549676	CL549676 OB_Ba008	1101	32.4	4.2	403	1	AA279393	AA279393 z855c10.s
C 1029	32.4	4.2	599	9	CE127342	CE127342 tigr-g8s-	1102	32.4	4.2	404	5	BP664904	BP664904 BP664904
C 1030	32.4	4.2	609	7	CF656333	CF656333 tacs3a12.	1103	32.4	4.2	413	1	AI446875	AI446875 EPM5060 E
C 1031	32.4	4.2	611	8	AZ426962	AZ426962 IM0208J06	1104	32.4	4.2	414	5	BQ452189	BQ452189 PFEST0aa9
C 1032	32.4	4.2	623	6	CD341634	CD341634 Str-Pu536.	1105	32.4	4.2	418	5	BQ452189	BQ452189 CH240_25H
C 1033	32.4	4.2	624	8	AZ271952	AZ271952 RPTC-23-4	1106	32.4	4.2	423	8	AG023353	AG023353 HS_2179_B
C 1034	32.4	4.2	630	7	CK654582	CK654582 AGENCOURT	1107	32.4	4.2	428	1	AL506360	AL506360 AL506360
C 1035	32.4	4.2	631	5	BQ186694	BQ186694 UI-E-EJ1-	1108	32.4	4.2	432	1	AL699258	AL699258 DKFZP6860
C 1036	32.4	4.2	635	8	AZ704651	AZ704651 RPTC-23-2	1109	32.4	4.2	432	2	BE362717	BE362717 DGI_88_C1
C 1037	32.4	4.2	639	6	CD322136	CD322136 Str-Pu537.	1110	32.4	4.2	435	2	BE645262	BE645262 7e67b12.x
C 1038	32.4	4.2	642	9	AG014549	AG014549 Homo sapi	1111	32.4	4.2	439	1	AL819598	AL819598 AL819598
C 1039	32.4	4.2	646	8	AZ703939	AZ703939 RPTC-23-2	1112	32.4	4.2	452	1	AV712380	AV712380 AV712380
C 1040	32.4	4.2	649	9	CR191634	CR191634 Forward s	1113	32.4	4.2	458	2	AW117866	AW117866 x83705.x
C 1041	32.4	4.2	654	8	BZ230879	BZ230879 CH230-476	1114	32.4	4.2	468	1	AL819085	AL819085 AL819085
C 1042	32.4	4.2	655	4	BU399291	BU399291 BJ399291	1115	32.4	4.2	469	2	AW183555	AW183555 X75H12.x
C 1043	32.4	4.2	658	9	CL589655	CL589655 OB_Ba009	1116	32.4	4.2	471	9	CG925126	CG925126 MBEFL61TR
C 1044	32.4	4.2	659	8	AQ415284	AQ415284 RPTC-11-1	1117	32.4	4.2	474	2	BE458935	BE458935 EST414227
C 1045	32.4	4.2	665	4	BM674327	BM674327 UI-E-EJ0-	1118	32.4	4.2	474	2	BE458935	BE458935 EST414227
C 1046	32.4	4.2	676	7	CN218914	CN218914 RJA041D10	1119	32.4	4.2	476	2	BE360184	BE360184 DGI_61_A1

1120	32.2	4.2	483	7	H59583	H59583 yr29f12.r1	1193	32.2	4.2	799	9	CR230522	Reverse s
1121	32.2	4.2	495	5	BX480191	BX480191 DXF2p686G	1194	32.2	4.2	802	5	CG966993	CG966993 MBECNA1TF
1122	32.2	4.2	496	2	BF574405	BF574405 602131617	1195	32.2	4.2	805	5	BW135784	BW135784
1123	32.2	4.2	497	7	CK512626	CK512626 rswd0_01	1196	32.2	4.2	807	2	BF028817	BF028817 601764778
1124	32.2	4.2	502	2	BE424118	BE424118 WHE0076_F	1197	32.2	4.2	812	6	CB678341	CB678341 OSJNBE16C
1125	32.2	4.2	503	8	AZ440820	AZ440820 1M0232001	1198	32.2	4.2	819	9	BX972981	BX972981 Reverse s
1126	32.2	4.2	504	4	BG946992	BG946992 IP1_2_C03	1199	32.2	4.2	828	9	CC517171	CC517171 CH240_363
1127	32.2	4.2	505	4	BG946992	BG946992 IP1_2_C04	1200	32.2	4.2	831	5	BU382156	BU382156 603860486
1128	32.2	4.2	506	8	AQ767932	AQ767932 HS_3089_A	1201	32.2	4.2	837	7	CK305054	CK305054 SB020274A
1129	32.2	4.2	519	6	CB678798	CB678798 OSJNBE01H	1202	32.2	4.2	842	5	BU307860	BU307860 603539737
1130	32.2	4.2	523	2	AW828046	AW828046 r861a02_Y	1203	32.2	4.2	847	5	BU794491	BU794491 SJF2CWA06
1131	32.2	4.2	523	2	BE879702	BE879702 601491796	1204	32.2	4.2	867	5	BU147852	BU147852 ENTQB64TF
1132	32.2	4.2	523	8	AQ833770	AQ833770 HS_5315_A	1205	32.2	4.2	886	9	BU147852	BU147852 ENTQB64TF
1133	32.2	4.2	529	5	BE786862	BE786862 BX768632	1206	32.2	4.2	896	9	CNS032XQ	CNS032XQ
1134	32.2	4.2	530	5	BQ596395	BQ596395 PFESToab3	1207	32.2	4.2	899	9	CG959519	CG959519 MBKJ26TR
1135	32.2	4.2	539	1	AI652367	AI652367 w660902.x	1208	32.2	4.2	902	8	AZ677735	AZ677735 ENLE14TF
1136	32.2	4.2	539	6	CD734523	CD734523 4048666_1	1209	32.2	4.2	911	9	CG547509	CG547509 CH240_430
1137	32.2	4.2	541	5	BU801309	BU801309 SJF2DBH01	1210	32.2	4.2	918	9	CG958349	CG958349 MBHT76TR
1138	32.2	4.2	545	5	BU779820	BU779820 SJF2DBH01	1211	32.2	4.2	919	9	CNS006NC	CNS006NC
1139	32.2	4.2	557	4	BG457346	BG457346 NF103F003P	1212	32.2	4.2	931	5	BU152317	BU152317 AGENCOURT
1140	32.2	4.2	567	8	BH328105	BH328105 CH230_45P	1213	32.2	4.2	941	5	BU795265	BU795265 SJF2DMF04
1141	32.2	4.2	567	9	CR495928	CR495928 Medicago	1214	32.2	4.2	953	3	CL792483	CL792483 OR_CBA000
1142	32.2	4.2	569	9	FR0025736	FR0025736 F_rubripe	1215	32.2	4.2	985	3	CR719563	CR719563 T8taadon
1143	32.2	4.2	585	1	AI795367	AI795367 605011H02	1216	32.2	4.2	1004	4	CG244503	CG244503 602356158
1144	32.2	4.2	585	7	CN127931	CN127931 RH0H1_26_	1217	32.2	4.2	1023	5	BX355747	BX355747 BX355747
1145	32.2	4.2	588	4	BJ040890	BJ040890 BJ040890	1218	32.2	4.2	1025	5	BQ676015	BQ676015 AGENCOURT
1146	32.2	4.2	594	4	BJ303164	BJ303164	1219	32.2	4.2	1038	7	CK205364	CK205364 FGAS01683
1147	32.2	4.2	600	4	BJ287188	BJ287188 BJ287188	1220	32.2	4.2	1043	4	BG482491	BG482491 602527271
1148	32.2	4.2	600	5	BQ539390	BQ539390 MEST615-D	1221	32.2	4.2	1054	8	CC257049	CC257049 CH261-42C
1149	32.2	4.2	606	7	CN140305	CN140305 OX1_35_G1	1222	32.2	4.2	1080	9	CNS006PP	CNS006PP
1150	32.2	4.2	607	9	CR498679	CR498679 Medicago	1223	32.2	4.2	1093	9	CNS05760	CNS05760
1151	32.2	4.2	613	8	AZ898966	AZ898966 RPEC1_24-2	1224	32.2	4.2	1132	5	BX402111	BX402111 BX402111
1152	32.2	4.2	617	5	BQ635428	BQ635428 1091070D0	1225	32.2	4.2	1132	5	BX402111	BX402111 BX402111
1153	32.2	4.2	619	8	BH300262	BH300262 CH230_109	1226	32.2	4.2	1340	3	CR620910	CR620910 full-leng
1154	32.2	4.2	621	9	CC740710	CC740710 ZMWBBb010	1227	32.2	4.2	1731	3	CR604240	CR604240 full-leng
1155	32.2	4.2	623	8	AQ471143	AQ471143 CTBT1-E1-	1228	32.2	4.2	3141	3	BC030234	BC030234 Homo sapi
1156	32.2	4.2	626	2	BE922735	BE922735 EST426504	1229	32.2	4.2	3565	3	HSMB03132	HSMB03132
1157	32.2	4.2	637	5	BQ172575	BQ172575 1091024E0	1230	32.2	4.2	242	6	CB974776	CB974776 CAB30005
1158	32.2	4.2	638	6	CF181319	CF181319 818131_MA	1231	32.2	4.2	270	5	BP507583	BP507583 BP507583
1159	32.2	4.2	639	5	BP166240	BP166240 BP166240	1232	32.2	4.2	280	2	BE664456	BE664456 148931_MA
1160	32.2	4.2	639	6	CB874431	CB874431 HX05D24W	1233	32.2	4.2	282	5	BP634093	BP634093 BP634093
1161	32.2	4.2	641	3	CR653070	CR653070 Tetrarodon	1234	32.2	4.2	314	1	AV239254	AV239254
1162	32.2	4.2	646	5	BF253320	BF253320 M1_MQ1_07	1235	32.2	4.2	315	2	BF388003	BF388003 UI-R-CA1-
1163	32.2	4.2	647	5	BW266341	BW266341 BW266341	1236	32.2	4.2	320	4	BM435669	BM435669 Iru8D1.ab
1164	32.2	4.2	650	7	CF925265	CF925265 M1_MQ1_07	1237	32.2	4.2	329	9	CR404678	CR404678 Arabidops
1165	32.2	4.2	656	8	AQ606140	AQ606140 CJT-HSP-2	1238	32.2	4.2	336	9	CD131373	CD131373 Arabidops
1166	32.2	4.2	657	7	CF518528	CF518528 DG9-18791	1239	32.2	4.2	338	6	CD131372	CD131372 MGI-0064T
1167	32.2	4.2	658	7	CF517560	CF517560 CAP0005_I	1240	32.2	4.2	359	4	BG407791	BG407791 dab23d11
1168	32.2	4.2	661	7	CF397053	CF397053 RYDS2_26_	1241	32.2	4.2	378	9	CR311593	CR311593 Medicago
1169	32.2	4.2	662	4	BJ303178	BJ303178 BJ303178	1242	32.2	4.2	394	1	AI432065	AI432065 th34902.x
1170	32.2	4.2	662	7	CK488081	CK488081 rswab0_00	1243	32.2	4.2	401	5	BY577961	BY577961 BY577961
1171	32.2	4.2	669	9	CL158220	CL158220 104_345_1	1244	32.2	4.2	406	9	BY577961	BY577961 Danio rer
1172	32.2	4.2	676	5	BU281579	BU281579 603600889	1245	32.2	4.2	407	8	AQ027483	AQ027483 CJT-HSP-2
1173	32.2	4.2	680	7	CK210385	CK210385 FGAS02219	1246	32.2	4.2	414	7	N73351	N73351 yv72b10.r1
1174	32.2	4.2	686	9	BX176061	BX176061 Danio rer	1247	32.2	4.2	422	9	BI184294	BI184294 Danio rer
1175	32.2	4.2	689	4	BJ539158	BJ539158 BJ539158	1248	32.2	4.2	453	2	BF961662	BF961662 QV2-NN004
1176	32.2	4.2	695	7	CF925058	CF925058 M1_MQ1_02	1249	32.2	4.2	461	2	AW406219	AW406219 UI-HF-BL0
1177	32.2	4.2	697	4	BJ310185	BJ310185 BJ310185	1250	32.2	4.2	472	8	BE107749	BE107749 UI-R-CAO-
1178	32.2	4.2	700	2	BE796759	BE796759 601587384	1251	32.2	4.2	475	8	CC456900	CC456900 SALK1013
1179	32.2	4.2	705	4	BJ309035	BJ309035 BJ309035	1252	32.2	4.2	485	8	BZ515704	BZ515704 BOMRK53TR
1180	32.2	4.2	709	7	CN134434	CN134434 OX1_26_G1	1253	32.2	4.2	488	2	BI198869	BI198869 UI-R-CAO-
1181	32.2	4.2	722	9	CB2379425	CB2379425 tigr-gss-	1254	32.2	4.2	490	8	B37654	B37654 HS-1044-B1-
1182	32.2	4.2	727	8	BZ022058	BZ022058 oee39502_	1255	32.2	4.2	496	9	BX127555	BX127555 Danio rer
1183	32.2	4.2	730	8	BH015255	BH015255 TDGBW82TH	1256	32.2	4.2	505	8	BZ116059	BZ116059 CH230-510
1184	32.2	4.2	731	5	BW158254	BW158254 BW158254	1257	32.2	4.2	513	6	CA240585	CA240585 SCSEFLA06
1185	32.2	4.2	734	7	CK769563	CK769563 957607_MA	1258	32.2	4.2	515	5	BM991659	BM991659 UI-H-Df1-
1186	32.2	4.2	740	9	AG451803	AG451803 Mus muscu	1259	32.2	4.2	517	8	AQ467042	AQ467042 HS_5192_B
1187	32.2	4.2	742	5	BG686763	BG686763 UI-CF-DU1	1260	32.2	4.2	518	6	CA602894	CA602894 wr1.pk000
1188	32.2	4.2	756	7	CR426111	CR426111 CH240_206	1261	32.2	4.2	535	9	CR104702	CR104702 Reverse s
1189	32.2	4.2	761	8	BZ856818	BZ856818 CH240_206	1262	32.2	4.2	536	4	BE593965	BE593965 W51_104_E
1190	32.2	4.2	762	5	BU18974	BU18974 SUM2CFC11	1263	32.2	4.2	536	4	BI799552	BI799552 HJ35A10_E
1191	32.2	4.2	772	5	BU140867	BU140867 603008177	1264	32.2	4.2	538	1	AV757416	AV757416 HJ35A10_E
1192	32.2	4.2	791	8	BZ391790	BZ391790 EINBW37TF	1265	32.2	4.2	545	7	CNS48536	CNS48536 EST_16174
										549	9	CE506899	CE506899 tigr-gss-

1266	32	4.2	553	8	A7722165	A7722165	RPCI-24-6	1339	32	4.2	863	9	CG970824	CG970824	MBEDS06TR
1267	32	4.2	559	4	B1290756	B1290756	UI-R-DK0-	1340	32	4.2	874	9	CR228736	CR228736	Forward s
1268	32	4.2	560	2	BF952030	BF952030	QV2-NN004	1341	32	4.2	874	9	CG064557	CG064557	FUJCK03TD
1269	32	4.2	562	7	CK824515	CK824515	ig27e03.Y	c1342	32	4.2	877	5	BU905384	BU905384	AGENCOURT
1270	32	4.2	566	1	AL594449	AL594449	AL594449	c1343	32	4.2	877	5	CG147800	CG147800	PUIHG69TD
1271	32	4.2	567	4	BJ046697	BJ046697	BJ046697	1344	32	4.2	896	8	AZ687152	AZ687152	ENTIX91TF
1272	32	4.2	568	5	BW335744	BW335744	BW335744	1345	32	4.2	924	5	CG088272	CG088272	FUJBR35TB
1273	32	4.2	575	9	CE348425	CE348425	tiGr-g8s-	1346	32	4.2	925	5	BU903869	BU903869	AGENCOURT
1274	32	4.2	586	5	BP027873	BP027873	BP027873	1347	32	4.2	933	4	BI410497	BI410497	603963187
1275	32	4.2	593	2	BE390303	BE390303	601286103	c1348	32	4.2	941	5	BU292092	BU292092	603607570
1276	32	4.2	594	8	B2220995	B2220995	CH230-467	1349	32	4.2	1001	9	AZ687340	AZ687340	ENTKS07TR
1277	32	4.2	595	4	BI180977	BI180977	BFUG1_002	c1350	32	4.2	1011	9	AL315360	AL315360	Tetraodon
1278	32	4.2	595	9	CE205854	CE205854	tiGr-g8s-	1351	32	4.2	1017	4	BMS60805	BMS60805	AGENCOURT
1279	32	4.2	600	8	BH441730	BH441730	BOHKB25TR	1352	32	4.2	1025	5	AL055840	AL055840	Drosophil
1280	32	4.2	601	8	BZ082860	BZ082860	11G84a01.	c1353	32	4.2	1027	5	BU134262	BU134262	603121030
1281	32	4.2	603	6	CA727822	CA727822	wd11c.pk0	1354	32	4.2	1037	8	CC231266	CC231266	Drosophil
1282	32	4.2	607	8	AQ760107	AQ760107	HS_2181.A	c1355	32	4.2	1085	8	CC231266	CC231266	CH261-32P
1283	32	4.2	611	6	CF213213	CF213213	CGF100063	c1356	32	4.2	1101	9	AO68607	AO68607	Drosophil
1284	32	4.2	614	6	CA755071	CA755071	BR0300120	c1357	32	4.2	1126	8	CC216546	CC216546	CH261-78J
1285	32	4.2	628	9	CR239534	CR239534	Forward s	1358	32	4.2	1189	6	CB588920	CB588920	AGENCOURT
1286	32	4.2	633	9	CR314109	CR314109	Medicago	c1359	32	4.2	1251	6	CD495791	CD495791	CDAL8-F04
1287	32	4.2	634	9	CL637973	CL637973	CH243-9G2	1360	32	4.2	1284	9	AG333588	AG333588	Mus muscu
1288	32	4.2	635	5	BU989807	BU989807	HF22M02r	c1361	32	4.2	1397	4	BG751380	BG751380	602730136
1289	32	4.2	643	2	BF296340	BF296340	03F8P06	1362	32	4.2	1955	9	AG278035	AG278035	Mus muscu
1290	32	4.2	646	6	CB176139	CB176139	pl18dl1.Y	1363	32	4.2	2244	3	CR699138	CR699138	Tetraodon
1291	32	4.2	650	5	BU996723	BU996723	HMI4116r	c1364	31.8	4.2	177	1	AI505294	AI505294	vgf6h12.x
1292	32	4.2	654	5	BU996533	BU996533	HMI3017r	c1365	31.8	4.2	199	4	BI966282	BI966282	1d50d03.x
1293	32	4.2	656	8	AZ568431	AZ568431	247PvA10	c1366	31.8	4.2	211	2	BB354729	BB354729	RST14570
1294	32	4.2	659	9	AG060382	AG060382	Pan trogl	c1367	31.8	4.2	213	4	BG195388	BG195388	RST14570
1295	32	4.2	665	9	CR152699	CR152699	Reverse s	c1368	31.8	4.2	278	7	CNS85563	CNS85563	USDA-FP.1
1296	32	4.2	666	5	BW302935	BW302935	BW302935	c1369	31.8	4.2	294	2	AW951272	AW951272	EST363342
1297	32	4.2	669	6	CB338971	CB338971	pl137b07.Y	1370	31.8	4.2	331	7	CR460477	CR460477	RC460477
1298	32	4.2	670	5	CB839922	CB839922	ZMMBBG049	c1371	31.8	4.2	334	7	CO867605	CO867605	Mdbb5010h
1299	32	4.2	671	9	BW370395	BW370395	BW370395	c1372	31.8	4.2	346	2	BE102793	BE102793	UI-R-BT1-
1300	32	4.2	674	2	BF365933	BF365933	P11_2_C03	1373	31.8	4.2	352	1	AA848610	AA848610	EST191370
1301	32	4.2	678	5	BW189805	BW189805	BW189805	1374	31.8	4.2	356	7	CK320290	CK320290	L3P02a02
1302	32	4.2	684	5	BW189735	BW189735	BW189735	1375	31.8	4.2	363	8	AQ205644	AQ205644	HS_3235_B
1303	32	4.2	685	5	BW984227	BW984227	UI-CF-EC1	c1376	31.8	4.2	378	2	BE926172	BE926172	PM1-BN017
1304	32	4.2	692	5	BW299580	BW299580	BW299580	1377	31.8	4.2	378	7	CN770741	CN770741	taf26f06.
1305	32	4.2	695	7	CR552646	CR552646	CR552646	1378	31.8	4.2	381	6	AZ357676	AZ357676	1M0099L21
1306	32	4.2	701	6	CA504839	CA504839	UI-R-R30-	1379	31.8	4.2	387	6	CB434520	CB434520	611142.MA
1307	32	4.2	703	4	BJ568434	BJ568434	BJ568434	1380	31.8	4.2	387	7	W81532	W81532	zh87C12.sl
1308	32	4.2	705	4	BG845276	BG845276	1024009E1	1381	31.8	4.2	391	1	AI249132	AI249132	qh79C05.x
1309	32	4.2	707	9	CR145607	CR145607	Forward s	1382	31.8	4.2	402	4	BM432565	BM432565	IJBUI1C10
1310	32	4.2	708	9	BX127358	BX127358	Danio rer	1383	31.8	4.2	404	6	CF134418	CF134418	CFG11-82.
1311	32	4.2	710	5	BW485785	BW485785	BW485785	c1384	31.8	4.2	407	4	BG604911	BG604911	WHE0944.H
1312	32	4.2	711	5	BW686404	BW686404	UI-CF-DU1	c1385	31.8	4.2	410	1	AA931390	AA931390	om98a02.s
1313	32	4.2	714	9	CC921944	CC921944	t060j13ba	c1386	31.8	4.2	417	1	AA460165	AA460165	zx60g12.s
1314	32	4.2	729	5	BU282051	BU282051	603867170	1387	31.8	4.2	425	8	AQ210977	AQ210977	HS_3237_A
1315	32	4.2	736	8	CC074345	CC074345	CSU-K33r.	c1388	31.8	4.2	436	1	AA670540	AA670540	vi02609.r
1316	32	4.2	739	9	CC519277	CC519277	RC240.366	1389	31.8	4.2	441	8	BH777145	BH777145	fzmb013f0
1317	32	4.2	754	4	BF982545	BF982545	602308154	1390	31.8	4.2	444	1	AI248625	AI248625	qh77b11.x
1318	32	4.2	755	8	B2462323	B2462323	BOQAA76TF	1391	31.8	4.2	448	7	CF803224	CF803224	rd95G04.Y
1319	32	4.2	757	4	BU569800	BU569800	BU569800	c1392	31.8	4.2	453	2	AW138892	AW138892	UI-H-B11-
1320	32	4.2	759	4	BU569057	BU569057	BU569057	c1393	31.8	4.2	460	7	CN651966	CN651966	cgWGRS
1321	32	4.2	762	9	AG612575	AG612575	Mus muscu	1394	31.8	4.2	462	1	AA179524	AA179524	zp48a11.f
1322	32	4.2	767	9	CR155232	CR155232	Reverse s	1395	31.8	4.2	467	8	AQ824044	AQ824044	HS_3141_A
1323	32	4.2	767	9	AG015348	AG015348	Homo sapi	1396	31.8	4.2	473	8	BH321410	BH321410	CH230-53E
1324	32	4.2	774	7	CN152465	CN152465	WOUNDI_82	c1397	31.8	4.2	476	8	AQ014209	AQ014209	RPCI11-20
1325	32	4.2	779	6	CB514741	CB514741	ssalrGB55	c1398	31.8	4.2	478	1	AA606783	AA606783	vm90a02.r
1326	32	4.2	779	9	CE101843	CE101843	tiGr-g8s-	c1399	31.8	4.2	479	7	DL6066	DL6066	RICC2766A.R
1327	32	4.2	781	8	BF085149	BF085149	11G96d08.	1400	31.8	4.2	482	4	BM429811	BM429811	1du021F3.
1328	32	4.2	787	9	CR103147	CR103147	Forward s	c1401	31.8	4.2	482	7	CN760890	CN760890	ID0AAA29D
1329	32	4.2	791	7	CN173332	CN173332	AGENCOURT	c1402	31.8	4.2	489	7	CN590229	CN590229	TTE000009
1330	32	4.2	819	4	BG822888	BG822888	602727884	1403	31.8	4.2	505	5	BM977275	BM977275	UI-CF-DU1
1331	32	4.2	821	4	BS548097	BS548097	601072338	1404	31.8	4.2	506	6	C97602	C97602	Rice
1332	32	4.2	824	8	CC345245	CC345245	OGMBP27TV	c1405	31.8	4.2	512	5	EX515758	EX515758	UX1-BC1P
1333	32	4.2	826	9	BX200514	BX200514	Danio rer	1406	31.8	4.2	516	7	CF529795	CF529795	EA1-BC1P
1334	32	4.2	838	7	CO398600	CO398600	AGENCOURT	c1407	31.8	4.2	517	5	BQ090146	BQ090146	rc62b04.Y
1335	32	4.2	841	7	CK751521	CK751521	963935.MA	c1408	31.8	4.2	519	2	BE429479	BE429479	TAS000.EI
1336	32	4.2	847	6	CB559180	CB559180	AGENCOURT	c1409	31.8	4.2	534	6	CD534966	CD534966	54L6.Arab
1337	32	4.2	848	7	CR804972	CR804972	AGENCOURT	c1410	31.8	4.2	535	8	AQ536694	AQ536694	RPCI-11-3
1338	32	4.2	857	7	CN227732	CN227732	RJB094F05	c1411	31.8	4.2	537	5	EX568099	EX568099	EX568099

1412	31.8	4.2	539	1	AL902953	AL902953	AL902953	1485	31.8	4.2	861	8	BH435554	BH435554 BOHPO60TF
1413	31.8	4.2	542	8	AZ300825	RF0123-1	AZ300825	1486	31.8	4.2	880	7	CN597766	CN597766 TTE000065
1414	31.8	4.2	547	5	BQ148466	NF068F03F	BQ148466	1487	31.8	4.2	888	9	CG814779	CG814779 SOYEN55TV
1415	31.8	4.2	551	6	CA646149	W4023G12-	CA646149	1488	31.8	4.2	889	2	BE967557	BE967557 601649083
1416	31.8	4.2	570	5	BQ553712	h023G12-	BQ553712	1489	31.8	4.2	892	2	BE878419	BE878419 601487817
1417	31.8	4.2	574	9	CE143202	tigr-g8s-	CE143202	1490	31.8	4.2	896	7	CN598625	CN598625 TTE000136
1418	31.8	4.2	579	7	CN651915	ES_CWGRS	CN651915	1491	31.8	4.2	899	5	BX761581	BX761581 TTE000136
1419	31.8	4.2	588	8	AQ179440	H8_3170_A	AQ179440	1492	31.8	4.2	900	6	CF238614	CF238614 AGENCOURT
1420	31.8	4.2	595	4	BM432303	1UEJ2G5.a	BM432303	1493	31.8	4.2	901	8	CU195073	CU195073 CH261-74E
1421	31.8	4.2	598	7	CN590493	TTE000110	CN590493	1494	31.8	4.2	902	5	BUI13873	BUI13873 603002367
1422	31.8	4.2	600	4	BI987259	3193-56 M	BI987259	1495	31.8	4.2	907	9	CG928202	CG928202 MBK145TR
1423	31.8	4.2	601	5	BQ306938	MR0-BT200	BQ306938	1496	31.8	4.2	908	9	CNS02X19	AL217782 Tetraodon
1424	31.8	4.2	604	8	AQ541403	RPCI-11-3	AQ541403	1497	31.8	4.2	921	6	CB203480	CB203480 AGENCOURT
1425	31.8	4.2	605	5	BZ210180	604155223	BZ210180	1498	31.8	4.2	930	9	CNS0047H	AL066358 Drosophila
1426	31.8	4.2	609	2	BE401797	CSB001C07	BE401797	1499	31.8	4.2	931	9	CG967648	CG967648 MBELES2TR
1427	31.8	4.2	609	5	BQ607390	BR1 3284	BQ607390	1500	31.8	4.2	942	9	CNS03FEU	AL241599 Tetraodon
1428	31.8	4.2	618	2	AW584702	N210816e	AW584702							
1429	31.8	4.2	630	7	CO354984	DR ATE NR	CO354984							
1430	31.8	4.2	638	8	BZ371066	ie30Q02.b	BZ371066							
1431	31.8	4.2	641	1	AL714522	AL714522	AL714522							
1432	31.8	4.2	645	8	AZ358485	IM0101N01	AZ358485							
1433	31.8	4.2	645	9	CE223050	tigr-g8s-	CE223050							
1434	31.8	4.2	651	6	CD901957	G356.105H	CD901957							
1435	31.8	4.2	664	4	BJ520261	RJ520261	BJ520261							
1436	31.8	4.2	666	8	AZ287549	RPCI-23-1	AZ287549							
1437	31.8	4.2	669	6	CA216623	SCCCFLU500	CA216623							
1438	31.8	4.2	672	5	BQ847521	Y BQ847521	BQ847521							
1439	31.8	4.2	673	5	BQ414021	GA_EG008	BQ414021							
1440	31.8	4.2	676	9	CE097126	tigr-g8s-	CE097126							
1441	31.8	4.2	682	5	BU008784	QSH8J13.Y	BU008784							
1442	31.8	4.2	685	7	CN625373	taes4e12.	CN625373							
1443	31.8	4.2	692	9	AG143793	Pan trogl	AG143793							
1444	31.8	4.2	693	1	AU129392	AU129392	AU129392							
1445	31.8	4.2	693	9	CG738178	MBMBB032	CG738178							
1446	31.8	4.2	695	6	CD935973	OV_102P20	CD935973							
1447	31.8	4.2	700	5	EX327419	EX327419	EX327419							
1448	31.8	4.2	700	5	CC543288	CH240_424	CC543288							
1449	31.8	4.2	706	6	CA222357	SCSGFL403	CA222357							
1450	31.8	4.2	707	8	AQ331213	nbxb0049C	AQ331213							
1451	31.8	4.2	708	7	CK983229	4098116 B	CK983229							
1452	31.8	4.2	719	5	BW386453	BW386453	BW386453							
1453	31.8	4.2	724	5	BQ177423	UI-M-ER0-	BQ177423							
1454	31.8	4.2	729	9	BX182008	Danio rer	BX182008							
1455	31.8	4.2	732	5	BQ056683	UI-H-ED0-	BQ056683							
1456	31.8	4.2	733	8	AZ190772	SP_1017 B	AZ190772							
1457	31.8	4.2	734	5	BQ850292	QGH12C24.	BQ850292							
1458	31.8	4.2	740	8	BZ074439	lj94c11.	BZ074439							
1459	31.8	4.2	741	9	CR306559	Medicago	CR306559							
1460	31.8	4.2	743	7	CO588621	DG2-22m16	CO588621							
1461	31.8	4.2	751	8	BZ071022	lk136D05.	BZ071022							
1462	31.8	4.2	753	9	AG352359	Mus muscu	AG352359							
1463	31.8	4.2	753	9	CN591468	TTE000094	CN591468							
1464	31.8	4.2	765	5	BW380634	BW380634	BW380634							
1465	31.8	4.2	772	1	AW006619	wt06a07.x	AW006619							
1466	31.8	4.2	774	8	BZ332521	IM0061J06	BZ332521							
1467	31.8	4.2	776	4	B1100924	60286247	B1100924							
1468	31.8	4.2	787	9	CG230982	Reverse s	CG230982							
1469	31.8	4.2	787	9	CG202325	ZMWBBc055	CG202325							
1470	31.8	4.2	794	2	BE778356	601463761	BE778356							
1471	31.8	4.2	799	7	CN592677	TTE000113	CN592677							
1472	31.8	4.2	807	7	CN593079	TTE000116	CN593079							
1473	31.8	4.2	807	7	CO200295	GE02_6 C1	CO200295							
1474	31.8	4.2	809	8	BZ267556	CH230-274	BZ267556							
1475	31.8	4.2	813	7	CN593498	TTE000063	CN593498							
1476	31.8	4.2	813	7	AZ199182	SP_1039 A	AZ199182							
1477	31.8	4.2	833	9	CC745649	ZMWBBB012	CC745649							
1478	31.8	4.2	834	8	BZ121741	CH230-411	BZ121741							
1479	31.8	4.2	835	8	CC100001	CSU-K34.1	CC100001							
1480	31.8	4.2	839	8	AQ863612	nbe0021K	AQ863612							
1481	31.8	4.2	840	8	BZ800128	PUGAV22TB	BZ800128							
1482	31.8	4.2	843	7	CN595404	TTE000087	CN595404							
1483	31.8	4.2	844	7	CN595444	TTE000133	CN595444							
1484	31.8	4.2	848	7	CN595698	TTE000072	CN595698							

ALIGNMENTS

RESULT 1
BC035754
LOCUS Homo sapiens, hypothetical protein FLJ22800, clone IMAGE:5760060, mRNA.
DEFINITION BC035754
ACCESSION BC035754
VERSION BC035754.1 GI:23242900
KEYWORDS HTC
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 2215)
AUTHORS Strausberg R.
TITLE Direct Submission
JOURNAL Submitted (31-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc.mgc@nih.gov
Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghigini, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q., Masello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantropop, S., Thomas, P.J., Touchman, J.W., Taurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 79 Row: 0 Column: 14
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 13376165
This clone has the following problem: retained intron.

FEATURES
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5760060"
/tissue_type="Colon, Kidney, Stomach, adult, whole pooled"

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/clone_lib="NIH_MGC_116"
/lab_host="DH10B"
/notes="Vector: pCMV-SPORT6"

ORIGIN
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Best Local Similarity 99.3%; Pred. No. 2.1e-201;
Matches 750; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 7 AGCGTTTCGACGAGGGTGACCATGACCTGCTCGAAGAGTGAACATCTCGAATGGA 66
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QY 67 TTCAGCGTCTGGTCTACTGCTGTAGAGTAGTTCCTCAATGCGATACCTCTAATTGTC 126
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Db 62 TTCAGCGTCTGGTCTACTGCTGTAGAGTAGTTCCTCAATGCGATACCTCTAATTGTC 121
   |||||
QY 127 AGCTTAGTTGAGAGAACCAATTTCTCAAAACCCCATCTCTGCTTGGTGGTTC 186
   |||||
Db 122 AGCTTAGTTGAGAGAACCAATTTCTCAAAACCCCATCTCTGCTTGGTGGTTC 181
   |||||
QY 187 CCAGGAATATAGGAGCAGGTCTGATGCGCATTCAGCAACAAACAAATGCTTCGACAGCA 246
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Db 182 CCAGGAATATAGGAGCAGGTCTGATGCGCATTCAGCAACAAACAAATGCTTCGACAGCA 241
   |||||
QY 247 AGAAAAAGAGCGTGTGCAACACAGAACTGGAATGTTTCTTCATCATTTTTTCAGTGTG 306
   |||||
Db 242 AGAAAAAGAGCGTGTGCAACACAGAACTGGAATGTTTCTTCATCATTTTTTCAGTGTG 301
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QY 307 ATCAGAGTCATTTGGTCTGTGTTATGATGATATCCATCCAGGCTCTCTTAAAGGT 366
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Db 422 ATCAGTGACATTCATCCAGAAATCCCTCAACTTGCAGTGGTTTTTCAATGATCTTTGCGCA 481
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Db 482 CCTCTCTACTGGTTTCAATAAACCCACAGTAACAGCACCATGCGGAGTGGTGGAGGCA 541
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QY 547 TCTAGTTTCCACTTCGATTTCAAGAAAAACAAACATAGGCTTATCCACTTCTCAGTATTT 606
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QY 607 TTAGGTCTATTGCTTGTGGAAATCTGGAGTCTCTGTTTGGGCTCAGTCAGATAGTCATC 666
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Db 602 TTAGGTCTATTGCTTGTGGAAATCTGGAGTCTCTGTTTGGGCTCAGTCAGATAGTCATC 661
   |||||
QY 667 GGTTCCTTGGCTGTCTGTGGAGTCTCTAAGCGAAGTAACAAATGCTAGTATTAAT 726
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Db 662 GGTTCCTTGGCTGTCTGTGGAGTCTCTAAGCGAAGTAACAAATGCTAGTATTAAT 721
   |||||
QY 727 GCGAATAAAATGTAAGTATCAGTAGTGTGAAAAA 761
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Db 722 GCGAATAAAATGTAAGTATCAGTAGTGTGAAATTA 756
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RESULT 2
BM923919
LOCUS
DEFINITION AGENCOURT 6709870 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5760060
5', mRNA sequence.
ACCESSION BM923919
VERSION BM923919.1 GI:19374298
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 995)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Straubeberg, Ph.D.
Email: cgaops-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Cloned through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMi2806 row: h column: 13
High quality sequence stop: 687.

FEATURES

source

1..995
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:5760060"
/lab_host="DH10B"
/clone_lib="NIH_MGC_116"
/note="Organ: pooled colon, kidney, stomach; Vector:
pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 96.1%; Score 736; DB 4; Length 995;
Best Local Similarity 99.2%; Pred. No. 2.3e-198;
Matches 750; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 7 AGCGTTTCGACGAGGGTGACCATGACCTGCTCGAAGAGTGAACATCTCGAATGGA 66
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Db 1 AACGTTTCGACGAGGGTGACCATGACCTGCTCGAAGAGTGAACATCTCGAATGGA 60
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QY 67 TTCAGCGTCTGGTCTACTGCTGTAGAGTAGTTCCTCAATGCGATACCTCTAATTGTC 126
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Db 61 TTCAGCGTCTGGTCTACTGCTGTAGAGTAGTTCCTCAATGCGATACCTCTAATTGTC 120
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QY 127 AGCTTAGTTGAGGAAGCAATTTTCTCAAAACCCCATCTCTGCTTGGTGGTTC 186
 |||||
Db 121 AGCTTAGTTGAGGAAGCAATTTTCTCAAAACCCCATCTCTGCTTGGTGGTTC 180
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QY 187 CCAGGAATATAGGAGCAGGTCTGATGCGCATTCAGCAACAAACAAATGCTTCGACAGCA 246
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Db 181 CCAGGAATATAGGAGCAGGTCTGATGCGCATTCAGCAACAAACAAATGCTTCGACAGCA 240
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QY 247 AGAAAAAGAGCGTGTGCAACACAGAACTGGAATGTTTCTTCATCATTTTTTCAGTGTG 306
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Db 241 AGAAAAAGAGCGTGTGCAACACAGAACTGGAATGTTTCTTCATCATTTTTTCAGTGTG 300
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QY 307 ATCAGTGACATTTGGTGTCTGTGTTATGATGATATCCATCCAGGCTCTCTTAAAGGT 366
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QY 367 CCTCTCATGTGTAATTTCTCAAGAACAGTAATGCAATTTGGAATTTTCATTGAAAAAC 426
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Db 361 CCTCTCATGTGTAATTTCTCAAGAACAGTAATGCAATTTGGAATTTTCATTGAAAAAC 420
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QY 427 ATCAGTGACATTCATCCAGAAATCCCTCAACTTGCAGTGGTTTTTCAATGATCTTTGCGCA 486
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Db 421 ATCAGTGACATTCATCCAGAAATCCCTCAACTTGCAGTGGTTTTTCAATGATCTTTGCGCA 480
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QY 487 CCTCCTACTGGTTTCAATTAACCCACAGTAACGACACCATGGAGTGGCTGGAGAGCA 546
Db 481 CCTCCTACTGGTTTCAATTAACCCACAGTAACGACACCATGGAGTGGCTGGAGAGCA 540
QY 547 TCTAGTTTCCACTTCCGATTTCTGAAGAAACCAACATAGGCTTATCCACTTCTCAGTATTT 606
Db 541 TCTAGTTTCCACTTCCGATTTCTGAAGAAACCAACATAGGCTTATCCACTTCTCAGTATTT 600
QY 607 TTAGGTTATTTGCTTGTGGAAATTTCTGGAGGCTCTGTGGGCTCAGTCAGATAGTCAATC 666
Db 601 TTAGGTTATTTGCTTGTGGAAATTTCTGGAGGCTCTGTGGGCTCAGTCAGATAGTCAATC 660
QY 667 GGTTCCTTGGCTCTGTGTGGAGTCTCTAAGCGAAGAAAGTCAAAATGTGTAGTTTAAAT 726
Db 661 GGTTCCTTGGCTCTGTGTGGAGTCTCTAAGCGAAGAAAGTCAAAATGTGTAGTTTAAAT 720
QY 727 GGGAAAT-AAATGTAAGTATCAGTAGTTTGAAGAAA 761
Db 721 GGGAAATAAATGTAAGTATCAGTAGTTTGAATAA 756

RESULT 3
CO581327
LOCUS
DEFINITION
ILLUMIGEN MQQ 47355 Katze MMJ Macaca mulatta cDNA clone
IBIUM:19521 5' similar to Bases 14 to 756 highly similar to human
FLJ22800 (Hs.156652), mRNA sequence.
ACCESSION
CO581327
VERSION
CO581327.1 GI:50412643
KEYWORDS
EST.
SOURCE
Macaca mulatta (rhesus monkey)
ORGANISM
Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
Cercopithecinæ; Macaca.
1. (Bases 1 to 856)
Katze,M.G., Thomas,M., Korth,M., Iadonato,S.P. and Magness,C.L.
Large-scale Rhesus Macaque cDNA Sequencing
Unpublished (2003)
Contact: C. Magness
Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408
Email: cmagness@illumigen.com
Sequenced on 2004.06.25. 762 Q20 bases. Library Preparation: Prof.
Michael Katze Lab at University of Washington DNA Sequencing:
Illumigen Biosciences Inc. For further information, see
http://www.macaque.org
PCR Primers
FORWARD: CCTCACTAAAGGGAACAAAA
BACKWARD: CACTATAGGGCGAATTGGGTA
Insert Length: 856 Std Error: 0.00
Plate: CL000433 row: B column: 01
Seq primer: CCTCACTAAAGGGAACAAAA
POLYA=Yes.

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/note="Organ: Jejunum; Vector: pDONR 222; Site 1: BsrG I;
Site 2: BsrG I; Created from CloneMiner cDNA Library
Construction kit (catalog #18249-029)"

ORIGIN
Query Match 87.7%; Score 671.8; DB 7; Length 856;

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Best Local Similarity 93.7%; Pred. No. 4.5e-180;
Matches 700; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 20 CAGGGGTGACCATGACCTGCTGGAGAGTGGACATCCTGCAATGGATTTCAGCCTGCTGG 79
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QY 80 TTCTACTGCTGTAGGAGTAGTTCTCAATGGGATACCTCTAAATTTGTGAGTTCAGTTAGG 139
Db 79 TTCTACTGCTGTAGGAGTAGTTCTCAATGGGATGCTCTAAATTTGTGAGTTCAGTTAGG 138
QY 140 AAGACCAATTTTCTCAAAACCCCATCTCTTTGAGTGGTGGTCCCAAGGAATTATAG 199
Db 139 AAGACCAATTTTCTCAAAACCCCATCTCTTTGAGTGGTGGTCCCAAGGAATTATAG 198
QY 200 GAGCAGGTCTGATGGCCATTTCCAGCAACAACATGTCTTGAACAAGAAAAAGAGCGT 259
Db 199 GAGCAGGTCTGATGGCCATTTCCAGCAACAACATGTCTTGAACAAGAAAAAGAGNAAT 258
QY 260 GCTGCAACAACAGAACTGGAAATGTTTCTTTCATCATTTTTTTCAGTGTGATCAGTCAATG 319
Db 259 GCTGCAACAACAGAACTGGAAATGTTTCTTTCATCATTTTTTTCAGTGTGATCAGTCAATG 318
QY 320 GTGCTCTGATTTGATGCTGATATCCATCCAGGCTCTCTTAAAGGTCCTCTCATGTGTA 379
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QY 380 ATTCTCCAAGCAACAGTAATGCCAATTTGCAATTTTTCATTTGAAAAACATCAGTGACATTC 439
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QY 500 TCAATTAACCCACAGTAACGACACCATGGGAGTGGCTGGAGAGCATCTAGTTCCACT 559
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QY 620 TTGTTGGAATTTCTGGAGTCTCTGTTGGGCTCAGTCAGATAGTCAATCGGTTTCTTGCT 679
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QY 680 GTCTGTGTGAGTCTCTAAGCGAAGAAAGTCAAAATTTGTAGTATTAATGGGAATAAATGT 739
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Db 739 AAGTATCAGTAGTTTGAAGAAAAA 765

RESULT 4
CO582275
LOCUS
DEFINITION
ILLUMIGEN MQQ 45967 Katze MMJ Macaca mulatta cDNA clone
IBIUM:16396 5' similar to Bases 13 to 834 highly similar to human
FLJ22800 (Hs.156652), mRNA sequence.
ACCESSION
CO582275
VERSION
CO582275.1 GI:50413995
KEYWORDS
EST.
SOURCE
Macaca mulatta (rhesus monkey)
ORGANISM
Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
Cercopithecinæ; Macaca.
1. (Bases 1 to 907)
Katze,M.G., Thomas,M., Korth,M., Iadonato,S.P. and Magness,C.L.
Large-scale Rhesus Macaque cDNA Sequencing

```

**JOURNAL
COMMENT**

Unpublished (2003)
Contact: C. Magness
Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Tel: 2063780400
Fax: 2063780408
Email: cmagness@illumigen.com
Sequenced on 2004.06.22. 655 Q20 bases. Library Preparation: Prof. Michael Katze Lab at University of Washington DNA Sequencing: Illumigen Biosciences Inc. For further information, see <http://www.macaque.org>
PCR Primers
FORWARD: CCCTCACTAAAGGGAACAAA
BACKWARD: CACTATAGGCGAATTGGGTA
Insert Length: 907 Std Error: 0.00
Plate: CL000377 row: B column: 06
seq primer: CCCTCACTAAAGGGAACAAA
polyA=No

FEATURES

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    /dev_stage="adult"
    /lab_host="Electronox DH10B"
    /clone_lib="Katze_MMJ"
    /note="Organ: Jejunum; Vector: pDONR 222; Site_1: BsrG I;
    Site 2: BsrG I; Created from Clonewiner cDNA Library
    Construction kit (catalog #18249-029)"

    84.5%; Score 647.4; DB 7; Length 907;
    Local Similarity 93.0%; Pred.No. 4.1e-17;
    609; Conservative 0; Mismatches 51; Indels 1; Gaps 1;

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ORIGIN

[illegible]

Qy	560	TCAATTCTGAAGAAAAAACAATACATAGGCTTATCCACTTCTCAGTAATTTTAGGTCTATTGC	619
Dd	558	TCAAATTCGTAAGAAAAAACAACACAGGCTCATCCAATCTCTCAGTCTTTTTTAGGTCTATTGC	617
Qy	620	TTGTTGGAAATTCGAGGTCCTGTTGGGCTCAGTCAGATAGTATCATCGTGTTCCTTGCGT	679
Dd	618	TTGTGGGAAATTCGAGGTCCTGTTGGGCTCAGTCAGATAGTATCATCGTGTTCCTTGCGT	677
Qy	680	GTCGTGTGGAGTCTCTAACGGAAGAAGTCAAAATTTGTGTAGTTTAATCGGGAATAAAAATGT	739
Dd	678	GTCGTGTGGAGTCTCTAACCGAA-AAATCAATTTGTAGTTTAATCGGGAATAAAAATGG	736
Qy	740	AAGTATCAGTAGTTTGAAAAA	760
Dd	737	AAGTATCAGTATTTTGAATAA	757
RESULT 5	CO644900	ILLUMIGEN MQO_43152 Katze MMUJ Macaca mulatta cDNA clone	linear EST 23-JUL-2000
LOCUS	DEFINITION	FBIUW:22282 5' similar to_Bases 16 to 824 highly similar to human	
ACCESSION	VERSION	FLJ22800 (HB.156652), mRNA sequence.	
KEYWORDS	SOURCE	Macaca mulatta (rhesus monkey)	
ORGANISM	REFERENCE	Katze,M.G., Thomas,M., Korth,M., Iadonato,S.P. and Magness,C.L. Large-scale Rhesus Macaque cDNA Sequencing Unpublished (2003) Contact: C. Magness Illumigen Biosciences Inc. 2203 Airport Way S, Suite 450, Seattle, WA 98134, USA Tel: 2063780400 Fax: 2063780408 Email: cmagness@illumigen.com Sequenced on 2004.06.05. 643 Q20 bases. Library Preparation: Prof. Michael Katze Lab at University of Washington DNA Sequencing: Illumigen Biosciences inc. For further information, see http://www.macaque.org PCR Primers FORWARD: CCCTCACTAAAGGGAACAAA BACKWARD: CACTATAGGCGCAATTGGTA Insert length: 924 Std Error: 0.00 Plate: CL000043 row: D column: 04 Seq primer: CCCTCACTAAAGGGAACAAA POLYA=No.	

FEATURES

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FEATURES
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    /clone_lib="Kazuo MMJ"
    /note="Organ: Jejunum; Vector: pDONR 222; Site 1: BsrG I;
    Site 2: BsrG I; Created from CloneMiner cDNA library
    Construction kit (catalog #19249-029)"

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ORIGIN

Query Match 83.9%; Score 642.6; DB 7; Length 924;
Best Local Similarity 92.6%; Pred. No. 9.7e-172;
Matches 686; Conservative 0; Mismatches 54; Indels 1; Gaps 1;

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QY 80 TTCTACTGCTGTTAGGAGTAGTTCTCAATCGATACCTCTAAATTGTCAGCTTAGTTGAGG 139
Db 81 TTCTACTGCTGTTAGGAGTAGTTCTCAATCGATACCTCTAAATTGTCAGCTTAGTTGAGG 140
QY 140 AAGACCAATTTTCTCAAAACCCCATCTCTTCTTCTGAGTGGTGTCTCCAGGAAATTATAG 199
Db 141 AAGACCGATCTCTCAAAACCCCATCTCTTCTTCTGAGTGGTGTCTCCAGGAAATTATAG 200
QY 200 GAGCAGTCTGATGGCCATCTTCAGCAACACATGCTCTTGCAGACGAGAAAGAGCGT 259
Db 201 GAGCAGTCTGATGGCCATCTTCAGCAACACATGCTCTTGCAGACGAGAAAGAGAAAT 260
QY 260 GCTGCAACACAGAACTGGAATGTTCTTCTCATCATTTTTCAGTGTGATCACAGTCATTG 319
Db 261 GCTGCAACACAGAACTGGAATGTTCTTCTCATCATTTTTCAGTGTGATCACAGTCATTG 320
QY 320 GTGCTCTGTATTGATGCTGATATCCATCCAGGCTCTCTTAAAGGTCTCTCATGTGTA 379
Db 321 GTGCTCTGTATTGATGCTGATATCCATCCAGGCTCTCTTAAAGGTCTCTCATGTGTA 380
QY 380 ATTCTCAAGCAACAGTAATGCAATTGTAATTTTCATTGAAACACATCAGTGACATTC 439
Db 381 ATTCTCAAGCAACAGTAATGCAATTGTAATTTTCATTGAAACACATCAGTGACATTC 440
QY 440 ATCCAGATCTCTCACTGCTGAGTGGTGTCTTCAATGACTCTTGTGACCTCTACTGGTT 499
Db 441 GCCCGGAAGACTCTCACTGCTGAGTGGTGTCTTCAATGACTCTTGTGACCTCTACTGGCT 500
QY 500 TCAATAAACCCACAGCAACACATGCGAGTGGCTGGAGAGCATCTAGTTTCCACT 559
Db 501 CCAAAACCCACAGCAACATGAGTCAAGCCAGCGCTGGAGAGCATCTAGTTTCCACT 560
QY 560 TCGATTCTGAAGAAAAACAAATAGGCTTATCCATCTTCAAGTATTTTAAAGTCTATTGC 619
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QY 620 TTGCTGGAATCTGAGGCTCTGTTGGGCTCAGTCAGATAGTCATCGGTTT-CCTTGGC 678
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QY 739 TAAGTATCAGTAGTTTGAATA 759
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RESULT 6
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LOCUS
DEFINITION BM923940 1006 bp mRNA linear EST 12-MAR-2002
5', mRNA sequence.
ACCESSION BM923940
VERSION BM923940.1 GI:19374319
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1006)
NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs@email.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.

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            female, 71 yo male colon; 46 yo male kidney, and pool of 2
            stomachs, 62 yo male and 70 yo female. Library is
            oligo-dT primed and directionally cloned (EcoRV site is
            destroyed upon cloning). Average insert size 1.4 kb,
            insert size range 1-3 kb. Library is normalized and
            enriched for full-length clones and was constructed by C.
            Gruber (Invitrogen). Research Genetics tracking code
            023. Note: this is a NIH_MGC Library."

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ORIGIN

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Query Match      82.8%; Score 634.6; DB 4; Length 1006;
Best Local Similarity 93.3%; Pred. No. 1.9e-169;
Matches 708; Conservative 0; Mismatches 44; Indels 7; Gaps 4;

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QY 69  CAGCCTGCTGGTTTCTACTGCTGTTAGGAGTGTCTCAATGCGATACCTCTTAATGTCAG 128
Db 62  GACCTGCTGGTTTCTACTGCTGTTAGGAGTGTCTCAATGCGATACCTCTTAATGTCAG 121
QY 129  CTTAGTGTGGAAGACAAATTTTCTCAAAACCCCATCTCTTGTGAGTGGTGGTCCC 188
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QY 189  AGGAATTAT----AGGAGCAGGTCTGATGGCCATTC-CAGCAACAACAATGTC-CTTGAC 242
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QY 243  AGCAAGAAAAAGAGCGTGTGCAACAACAGAACTGGAATGTTTCTTTCATCATTTTTTCAG 302
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QY 303  TGTGATCAGATCATTTGGTGTCTGTATGTCATGCTGATATCCATCCAGGCTCTCTTAAA 362
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QY 363  AGGTCTCTCATGTGTAATTTCTCAAGCAACAGTAATGCCAATGTGAAATTTTCATTGAA 422
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QY 423  AAAACATCAGTGACATTCATCCAGAACTCTTCAACTTGCAGTGGTGTTCATGACTCTTG 482
Db 421  AAAACATCAGTGACATTCATCCAGAACTCTTCAACTTGCAGTGGTGTTCATGACTCTTG 480
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Db 481  TGCACCTCTTACTGTTTCAATAAACCCAGTAAAGACACCATCGCGAGTGGTGGAG 540
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
 Plate: LNL12806 Row: i Column: 13
 High quality sequence start: 251
 High quality sequence stop: 702.

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QY 663 CATCGGTTTCTGCTGCTGTGTGGAGTCTCTAAGCGAAGAAGTCAAATTGTGTAGTT 722
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RESULT 7
CO582384
LOCUS
DEFINITION
ILLUMIGEN MCQ_45837 Katze MMJ Macaca mulatta cDNA clone
FLJ22800 (Hs.156652), mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Macaca mulatta (rhesus monkey)
Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
Cercopitheciinae; Macaca.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
1 (bases 1 to 896)
Katze, M.G., Thomas, M., Korth, M., Iadonato, S.P. and Magnus, C.L.
Large-scale Rhesus Macaque cDNA Sequencing
Unpublished (2003)
Contact: C. Magnus
Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408
Email: cmagnus@illumigen.com
Sequenced on 2004.06.22. 521 Q20 bases. Library Preparation: Prof.
Michael Katze Lab at University of Washington DNA Sequencing:
Illumigen Biosciences Inc. For further information, see
http://www.macaque.org

PCR Primers
BACKWARD: CCTCACTAAAGGGAACAAA
FORWARD: CACTATAGGCGCAATGGGTA
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POLYA=NO.

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Site 2: BsrG I; Created from Cloneminer cDNA Library
Construction kit (catalog #18249-029)"

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Best Local Similarity 91.1%; Pred. No. 1.7e-162; Indels 0; Gaps 0;
Matches 648; Conservative 0; Mismatches 63;
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QY 86 TGCTGTAGGAGTAGTCTCTCAATGCGATACCTCTTAATGTCAGCTTAGTTAGGAGGACC 145

Db 62 TGCTGTAGGAGTAGTCTCAATGCGATGCTCTAAATTGTCAGCTTAATTAGGAGGACC 121
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QY 326 TGTAATTCATGCTGATATCCATCCAGGCTCTCTTAAAGGTCCTCTCATGTGTAATTTCTC 385
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QY 446 AATCTTCAACTTCAGTGTGTTTTCATGACTCTTTCAGTGTGATCACAGTCAATGGTGCTC 505
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QY 506 AATCTTCAACTTCAGTGTGTTTTCATGACTCTTTCAGTGTGATCACAGTCAATGGTGCTC 565
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QY 686 GTGAGGCTCTTAAGCGAAGAAGTCAAAATGTTGTAATTTTAATGGGAATAAAA 736
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RESULT 8
CN793461
LOCUS
DEFINITION
4128489 BARC 8BOV Bos taurus cDNA clone 8BOV_48115 5', mRNA
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Bos taurus (cow)
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE
AUTHORS
Baumann, R.G., Baldwin, R.L., Sonstegard, T.S., Van Tassell, C.P. and
Marukamalli, L.K.
Construction and Analysis of a cDNA Library Generated From
Intestinal Muscle and Epithelial Tissues of Holstein Cattle
Unpublished (2004)
Contact: Richard G. Baumann
Bovine Functional Genomics Lab
ANR
BLDG 162; BARC-EAST, Beltsville, MD 20705, USA
Tel: 3015048604
Fax: 3015048744
Email: rbaumann@anri.barc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
0.000925 using options -trim alt -, -trim fasta. Vector identified
by cross_match using options -minmatch 12 -minscore 18

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/lab_host="DH10B Tona"
/clone_lib="BARC 8BOV"
/notes="Organ: Intestine; Vector: pCMVSPORT6.1; Site 1:
NotI; Site 2: EcoRI; Normalized cow cDNA intestinal
library in pCMVSPORT6.1, constructed from equimolar mRNA
pools derived from 5 sources, 4 lactating intestinal, 1
neonatal intestinal 4/5 Lactating, Proximal Duodenum,
Jejunum, Distal Ileum, Colon, 1/5 Neonatal, Proximal
Duodenum, Jejunum, Distal Ileum"
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RESULT 9
COS80240
LOCUS
DEFINITION
COS80240 888 bp mRNA linear EST 20-JUL-2004
ILLUMIGEN MCQ_48946 Katze MMDD Macaca mulatta cDNA clone
IBIUM:18267 5' similar to Bases 212 to 788 highly similar to human
FLJ22800 (Hs.156652), mRNA sequence.

ACCESSION
COS80240
VERSION
COS80240.1 GI:50411340
KEYWORDS
EST.
SOURCE
Macaca mulatta (rhesus monkey)
ORGANISM
Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
Cercopitheinae; Macaca.

REFERENCE
1 (bases 1 to 888)
Katze, M.G., Thomas, M., Korth, M., Iadonato, S.P. and Magness, C.L.
Large-scale Rhesus Macaque cDNA Sequencing
Unpublished (2003)
Contact: C. Magness
Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408
Email: cmagness@illumigen.com

AUTHORS
Michael Katze Lab at University of Washington DNA Sequencing:
Illumigen Biosciences Inc. For further information, see
http://www.macaque.org

JOURNAL
PCR Primers
FORWARD: CCTCACTAAAGGGAACAAA
BACKWARD: CACTATAGGCGGAATTGGTA
Insert Length: 888 Std Error: 0.00
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Site 2: BsrG I; Created from CloneMiner cDNA Library
Construction kit (catalog #18249-029)"

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Best Local Similarity 84.5%; Pred. No. 3e-129;
Matches 607; Conservative 0; Mismatches 44; Indels 67; Gaps 2;
QY 20 CAGGGGTGACCATGACCTGCTGGGAAGGATGGACATCCTGCAATGCAATTCAGCTGCTGCTGG 79
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QY 140 AAGACCAATTTTCTCAAAACCCCATCTCTTGTCTTGTAGTGGTGGTTCACAGGAATTATAG 199
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Best Local Similarity 82.0%; Pred. No. 5.7e-130;
Matches 584; Conservative 0; Mismatches 125; Indels 3; Gaps 1;
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QY 614 TATTGCTTGTGGAATTTCTGGAGTCTCTGTTTGGGCTCAGTCAGATAGTCAATCGGTTTCC 673
DB 602 TACTGCTTGTGGCATCTCGAGATTTCTGTTGGACTCAGTCAGATTAATCATCGGCTTCT 661
QY 674 TTGGCTGTCTGTGT---GGAGTCTCTAAAGCGAAGAGTCAAAATTTGTGTAGTT 722


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623 TTGGAAATCTCGAGCTCTCTTTGGGCTCAGTCAGATAGTCATCGGTTTCTTGGCTGTC 682
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743 TATCAGTAGTTTGAATAA 760
739 TATCAGTAGTTTGAATAA 756

RESULT 14
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LOCUS
DEFINITION
BY707590 RIKEN full-length enriched, 10 day old male pancreas Mus
musculus cDNA clone 1810018L02 5', mRNA sequence.
BY707590
EST.
BY707590.1 GI:27118767
Mus musculus (house mouse)
ORGANISM
REFERENCE
AUTHORS
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 972)
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Osato, R., Saito, R., Suzuki, H., Yamanaka, I.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,
Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,
Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusci, V.,
Chochia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,
Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,
Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
Gustinich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,
Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konggaya, A.,
Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,
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Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,
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Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,
Welle, C., Wilming, L.G., Wyszewski, B., Yang, I., Yang, I.,
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,
Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,
Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
12456851
12466851
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P.,
Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F.,
Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y.,
Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M.,
Nomura, K., Numazaki, R., Ohno, M., Oheato, N., Saito, R., Sakazume, N.,
Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M.,
Takeda, Y., Waki, K., Watanaka, A., Muramatsu, M. and Hayashizaki, Y.

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Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
FEATURES
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pancreas"
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Best Local Similarity 80.8%; Pred. No. 1.3e-123;
Matches 594; Conservative 0; Mismatches 127; Indels 14; Gaps 3;
Qy 23 GGGTGCACATGACCTGCTGGGAAGATGGAGCATCTGCAATGGATTCAGCGCTGCTGTTTC 82
Db 29 GGAACCATGATGCTGCTGGAGGGTGGACATCTGCAATGGCTTCAGCGCTGCTCATTC 88
Qy 83 TACTGCTGTAGGAGTAGTTCTTCAATGCGATACCTCTAATTTGTACGCTTAGTTAGGAG 142
Db 89 TGATCTGCTAGGAGTAGTTCTAATCAATTTGTATACCCCTGGGAATAGCTTAGTGGAGG 148
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Qy 203 CAGTCTGTATGGCCATTCAGACCAACAATGTCTTGCACAGCAAGAAAGAGCGTGCT 262
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Qy 263 GCACACACAGACTGGATGTTCTTTCATCATCTTTTCAGTGTGATCAGTCATTTGG 322
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